



1133934_1.TXT
SEQUENCE LISTING

<110> Ullman, Katharine
Liu, Jin
Prunuske, Amy
Dimaano, Christian

<120> METHODS OF INHIBITING CELL CYCLE OF A CELL COMPRISING ADMINISTERING
A NUP153 INHIBITOR

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<140> 10/528183
<141> 2005-05-27

<150> PCT/US2003/29267
<151> 2003-09-17

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<160> 106

<170> PatentIn version 3.5

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Note = Synthetic Construct

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35 40 45

Asn Ile Val Pro Gly Trp Leu Gln Arg Tyr Phe Asn Lys Asn Glu Asp
50 55 60

Val Cys Ser Cys Ser Thr Asp Thr Ser Glu Val Pro Arg Trp Pro Glu
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65

Asn Lys Glu Asp His Leu Val Tyr Ala Asp Glu Glu Ser Ser Asn Ile
85 90 95

Thr Asp Gly Arg Ile Thr Pro Glu Pro Ala Val Ser Asn Thr Glu Glu
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Pro Ser Thr Thr Ser Thr Ala Ser Asn Tyr Pro Asp Val Leu Thr Arg
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Asp Asp Asp Asn Ile Ser Thr Thr Ser Gly Phe Ser Ser Arg Ala Ser
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Asp Lys Asp Ile Thr Val Ser Lys Asn Thr Ser Leu Pro Pro Leu Trp
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Ser Pro Glu Ala Glu Arg Ser His Ser Leu Ser Gln His Thr Ala Thr
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Ser Ser Lys Lys Pro Ala Phe Asn Leu Ser Ala Phe Gly Thr Leu Ser
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Pro Ser Leu Gly Asn Ser Ser Ile Leu Lys Thr Ser Gln Leu Gly Asp
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Ser Pro Phe Tyr Pro Gly Lys Thr Thr Tyr Gly Gly Ala Ala Ala Ala
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Val Arg Gln Ser Lys Leu Arg Asn Thr Pro Tyr Gln Ala Pro Val Arg
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Arg Gln Met Lys Ala Lys Gln Leu Ser Ala Gln Ser Tyr Gly Val Thr
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Ser Ser Thr Ala Arg Arg Ile Leu Gln Ser Leu Glu Lys Met Ser Ser
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Pro Leu Ala Asp Ala Lys Arg Ile Pro Ser Ile Val Ser Ser Pro Leu
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Asn Ser Pro Leu Asp Arg Ser Gly Ile Asp Ile Thr Asp Phe Gln Ala
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Lys Arg Glu Lys Val Asp Ser Gln Tyr Pro Pro Val Gln Arg Leu Met
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Thr Pro Lys Pro Val Ser Ile Ala Thr Asn Arg Ser Val Tyr Phe Lys
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Pro Ser Leu Thr Pro Ser Gly Glu Phe Arg Lys Thr Asn Gln Arg Ile
 385 390 395 400

Asp Asn Lys Cys Ser Thr Gly Tyr Glu Lys Asn Met Thr Pro Gly Gln
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Asn Arg Glu Gln Arg Glu Ser Gly Phe Ser Tyr Pro Asn Phe Ser Leu
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Pro Ala Ala Asn Gly Leu Ser Ser Gly Val Gly Gly Gly Gly Gly Lys
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Glu Glu Met Glu Val Pro Val Leu Pro Lys Ile Ser Leu Pro Ile Thr
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Gln Met Thr Ser Pro Ser Ser Thr Gly Ser Pro Met Phe Lys Phe Ser
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Ser Pro Ile Val Lys Ser Thr Glu Ala Asn Val Leu Pro Pro Ser Ser
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Ile Gly Phe Thr Phe Ser Val Pro Val Ala Lys Thr Ala Glu Leu Ser
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Gly Ser Ser Ser Thr Leu Glu Pro Ile Ile Ser Ser Ser Ala His His
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Cys Glu Gly Pro Phe Arg Pro Ala Glu Ile Leu Lys Glu Gly Ser Val
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Leu Asp Ile Leu Lys Ser Pro Gly Phe Ala Ser Pro Lys Ile Asp Ser
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Val Ala Ala Gln Pro Thr Ala Thr Ser Pro Val Val Tyr Thr Arg Pro
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Ala Ile Ser Ser Phe Ser Ser Ser Gly Ile Gly Phe Gly Glu Ser Leu
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Val Thr Asp Asn Lys Cys Ile Ala Cys Gln Ala Ala Lys Leu Ser Pro
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Arg Asp Thr Ala Lys Gln Thr Gly Ile Glu Thr Pro Asn Lys Ser Gly
690 695 700

Lys Thr Thr Leu Ser Ala Ser Gly Thr Gly Phe Gly Asp Lys Phe Lys
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Pro Val Ile Gly Thr Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys
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Pro Glu Ala Ile Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr
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Cys Val Lys Arg Ala Leu Thr Leu Thr Val Val Ser Glu Ser Ala Glu
755 760 765

Thr Met Thr Ala Ser Ser Ser Ser Cys Thr Val Thr Thr Gly Thr Leu
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Gly Phe Gly Asp Lys Phe Lys Arg Pro Ile Gly Ser Trp Glu Cys Ser
785 790 795 800

Val Cys Cys Val Ser Asn Asn Ala Glu Asp Asn Lys Cys Val Ser Cys
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Met Ser Glu Lys Pro Gly Ser Ser Val Pro Ala Ser Ser Ser Ser Thr
820 825 830

Val Pro Val Ser Leu Pro Ser Gly Gly Ser Leu Gly Leu Glu Lys Phe
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Lys Lys Pro Glu Gly Ser Trp Asp Cys Glu Leu Cys Leu Val Gln Asn
850 855 860

Lys Ala Asp Ser Thr Lys Cys Leu Ala Cys Glu Ser Ala Lys Pro Gly
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Thr Lys Ser Gly Phe Lys Gly Phe Asp Thr Ser Ser Ser Ser Ser Asn
885 890 895

Ser Ala Ala Ser Ser Ser Phe Lys Phe Gly Val Ser Ser Ser Ser Ser
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Gly Pro Ser Gln Thr Leu Thr Ser Thr Gly Asn Phe Lys Phe Gly Asp
915 920 925

Gln Gly Phe Lys Ile Gly Val Ser Ser Asp Ser Gly Ser Ile Asn
930 935 940

Pro Met Ser Glu Gly Phe Lys Phe Ser Lys Pro Ile Gly Asp Phe Lys
945 950 955 960

Phe Gly Val Ser Ser Glu Ser Lys Pro Glu Glu Val Lys Lys Asp Ser
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Lys Asn Asp Asn Phe Lys Phe Gly Leu Ser Ser Gly Leu Ser Asn Pro
980 985 990

Val Ser Leu Thr Pro Phe Gln Phe Gly Val Ser Asn Leu Gly Gln Glu
995 1000 1005

Glu Lys Lys Glu Glu Leu Pro Lys Ser Ser Ser Ala Gly Phe Ser
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Phe Gly Thr Gly Val Ile Asn Ser Thr Pro Ala Pro Ala Asn Thr
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Glu Thr Lys Ser Ala Ser Val Ala Pro Phe Thr Cys Lys Thr Ser
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Glu Ala Lys Lys Glu Glu Met Pro Ala Thr Lys Gly Gly Phe Ser
Page 8

1070

1075

1080

Phe Gly Asn Val Glu Pro Ala Ser Leu Pro Ser Ala Ser Val Phe
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 1100 1105 1110

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Glu Asn Ser Ser Lys Ser Thr Phe Ser Phe Ser Met Thr Lys Pro
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Val Phe Thr Phe Gly Ala Asn Ser Ser Thr Pro Ala Ala Ser Ala
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Gln Pro Ser Gly Ser Gly Gly Phe Pro Phe Asn Gln Ser Pro Ala
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Ala Phe Thr Val Gly Ser Asn Gly Lys Asn Val Phe Ser Ser Ser
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<223> Description of Artificial Sequence: Note = Synthetic Construct

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<223> Description of Artificial Sequence: Note = Synthetic Construct

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| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ile | Arg | Ser | Arg | Arg | Tyr | His | Leu | Ser | Ser | Gly | Arg | Thr | Pro | Tyr |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Lys | Ser | Arg | Gln | Arg | Gln | Gln | Gly | Ile | Ile | Ser | Arg | Val | Thr | Asp |
| | | 35 | | | | 40 | | | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Lys | Ser | Ile | Val | Pro | Gly | Trp | Leu | Gln | Lys | Tyr | Phe | Asn | Lys |
| | 50 | | | | | 55 | | | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Glu | Glu | Glu | His | Asp | Arg | Val | His | Ser | Ala | Ser | Glu | Val | Ile | Val |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |

Asn Asp Thr Glu Ala Arg Glu Asn Asn Ala Gln His His Ile Tyr Asp
85 90 95

Asp Asp Asp Glu Glu Gly Asn Ser Pro Thr Asp Gly Arg Val Thr Pro
100 105 110

Glu Pro Val Ile Asn Val Asp Glu Glu Val Pro Ser Thr Ser Gln Ser
115 120 125

Ala Ile Asn Asn Thr Asp Ala Leu Thr Arg Pro Ser Leu His Arg Ala
130 135 140

Ser Leu Asn Phe Asn Ile Phe Asp Ser Pro Ala Leu Asn Cys Gln Pro
145 150 155 160

Ser Thr Ser Ser Ala Phe Pro Ile Gly Thr Ser Gly Phe Ser Leu Ile
165 170 175

Lys Glu Ile Lys Asp Ser Thr Ser Gln His Asp Asp Asp Asn Ile Ser
180 185 190

Thr Thr Ser Gly Phe Thr Ser Arg Ala Ser Asp Lys Asp Leu Ala Val
195 200 205

Ser Lys Asn Val Ser Val Pro Pro Leu Trp Ser Pro Glu Val Asp Arg
210 215 220

Ser Gln Ser Leu Ser His Asn Ser Ser Met Thr Ser Lys Lys Pro Thr
225 230 235 240

Phe Asn Leu Ser Ala Phe Gly Ser Leu Ser Pro Ser Leu Gly Asn Ala
245 250 255

Ser Ile Leu Asn Arg Gln Leu Gly Asp Ser Pro Phe Tyr Pro Gly Lys
260 265 270

Thr Thr Tyr Gln Gly Ala Ala Ala Val Arg Ser Ser Arg Val Arg Ala
275 280 285

Thr Pro Tyr Gln Ala Pro Leu Arg Arg Gln Val Lys Ala Lys Pro Ala
290 295 300

Ala His Ser Gln Gln Cys Gly Val Thr Ser Ser Ala Ala Arg Arg Ile
305 310 315 320

Leu Gln Ser Leu Glu Lys Met Ser Ser Pro Leu Ala Asp Ala Lys Arg

Ile Pro Ser Asn Ser Ser Leu Ser His Thr Pro Glu Lys Asn Val Met
340 345 350

Asp Ile Pro Glu Asn Pro Ser Lys Arg Lys Lys Val Glu Ser Pro Phe
355 360 365

Pro Pro Val Gln Arg Leu Val Thr Pro Lys Ser Ile Ser Val Ser Ala
370 375 380

Asn Arg Ser Leu Tyr Ile Lys Pro Ser Leu Thr Pro Ser Ala Val Ser
385 390 395 400

<210> 5

<211> 4305

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 5

| | |
|--|------|
| cgcaaaccgt tccctgtata tcaagccttc actgacacca tctgctgtat caaatacaaa | 60 |
| cagtcgcaga atacagccag acaagcacia tgagtcacaa aagaataatc tgcaatcaac | 120 |
| atctcagtct cacagcttct cttacccaaa gttcagtact ccggcatcca atggattgtc | 180 |
| atcaggaaca ggtggtggca aaatgatgag ggaaaaaggc tctcattact caacaaagcc | 240 |
| agctaattgag gagctggatg ggcctgtttt acctgaaatc ccattgcctc ttagcacagc | 300 |
| agcccttccc agctttcaat tttcaacttt gtctggctct gctacttcgc ctatctctgt | 360 |
| cactaaacct gcaaacagta cgacatgtca ctttaaccagc agtagtccat cgttcacatt | 420 |
| ttcgtcccct attgtaaaat cgactgaatc aaatgctcag ttttctggct catctgttga | 480 |
| tttcactttc agtgtaccag cagcgaaagc gtcacttgca acatctgatg agagcaaggc | 540 |
| gtctgctgta agtagcgagg ctaaaacaca tgctgctgtt aatagcagtg caaagaacac | 600 |
| tgatgatgaa caagtgggat tctgtaaacc tgcaaaaact ctgaaggaag ggagtgtgtt | 660 |
| agacatgctg agaagtccag ggttttcttc tttaccctcc ctgctaactt cagaatcaac | 720 |
| tcttaacaga agcacaccaa ccctctcaaa gactgtgggg aatacattct cccctgcaaa | 780 |
| tgtatcatta ggagtaggaa gcaagcaatt tggactttgg caatgcagcg catgctttca | 840 |
| tgagaatatg tcatctgata gcaactgtat ttcttgctct gctgtaaaac ctcggcctac | 900 |
| agaaacctct aagaaactac ctgcttcacc accaagtagc aatacaaaaa gcactgtccc | 960 |
| actttctagc acaccaggac taggagacat atttaaaaaa cctgcaggca tgtgggattg | 1020 |
| tgacacttgt ttagtacaga acaaagcaga agtaacaaaa tgtgttgctt gtgaaacccc | 1080 |

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| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| caaacctggg | acttgataa | aagctacctt | gttgataccg | tccaccacaa | agtctataaa | 1140 |
| tccagccaca | aatacccttg | cttttgcac | ttgctctgca | agcattccaa | atgaagaaat | 1200 |
| gttcaaaaag | cctatgggat | cttgggagtg | cacagtttgt | catatgcaga | ataaaacaga | 1260 |
| ggataataca | tgtgtgggct | gcaaagctga | gaaaccagga | accgtcaaga | gcgtacctac | 1320 |
| tgctgcacca | tcagggctgc | tgggatttgt | acatcagttt | aaaaaaccaa | cagggagctg | 1380 |
| ggatttgtgat | gtctgcttaa | tacaaaacaa | accagaagcc | gccaaatgta | ttgcatgtga | 1440 |
| aagtgccaaa | ccaggcacca | aagcagaacc | gaaaggact | tttgatacag | tgaaaaattc | 1500 |
| cgtttcagtt | gcaccccttt | cttcagggca | gctgggattg | ttagatcagt | ttaagaagtc | 1560 |
| ggcaggaagc | tgggatttgt | atgtctgcct | agtagaaaac | aaaccagaag | ccacaaaatg | 1620 |
| tgttgcctgt | gagacctcaa | aaccaggcac | aaaagcagaa | ttaaaagggt | ttggaacatc | 1680 |
| aaccttttcc | tctggaacag | cagctccgac | cttcaagttt | ggtgtgcagt | cttcagatag | 1740 |
| cactgctgag | ttaaaatcgg | gtgcctctac | aagtggtttt | gccaaatcta | taggggattt | 1800 |
| taaatttggg | ttagtgtctg | catccacaac | aacagaggaa | actggcaaga | aaagctttac | 1860 |
| atttggctct | tctactacca | atgaagtttc | agcaggtttt | aagtttggca | ttgccggttc | 1920 |
| tgctcagaca | aaaccagaca | ccctaagtca | gtctaccaca | agtggtttca | catttggttc | 1980 |
| tgtttccaac | acggtttctc | ttgctcctgc | tgcaactagc | tcatcgagta | caggcttgca | 2040 |
| agtggcggct | gcaattgctg | attccaacct | tgcaactact | gctgccttga | aatcagcaga | 2100 |
| agagaaaaag | gccgaagcac | ctacaataac | accgttttct | tttgggaaaa | cagatcaaaa | 2160 |
| taaagagact | gcatccacct | cttttgtctt | tggaaagaaa | gatgaaaaga | cagactctgc | 2220 |
| tccaactgga | tcttcctttg | cttttgggct | aaaaaaggat | ggggaggaat | ctaagccgtt | 2280 |
| tctttttgga | aaacctgagc | caaccaaaag | agatggcaat | gcagcatctg | ctggttttgc | 2340 |
| ttttggtgtg | actaatccca | cagagaaaaa | ggatattgaa | cagcctggaa | aatcagtttt | 2400 |
| tgcttccggt | gctcaaactt | caatcacaga | tgctggagct | tccaagcaac | cttttagttt | 2460 |
| tctgaccaat | gtctcctcca | ctgcagcttc | atcaagcact | tgtggtgttt | ccagcagtgt | 2520 |
| atttggcagt | gtgactcagt | caagcactcc | tgcaaccctt | agtaatgtgt | ttggcagtgc | 2580 |
| tatttcagca | aatgctcctg | ccccgtctag | tggtgtattt | ggaaacctca | ctccatcaaa | 2640 |
| tgcccctgca | gcttctagca | ctttgtttgg | taacgttgct | ccctcaagta | ctccttctgg | 2700 |
| ctccagtggg | ttgtttggca | ctgcagctgc | atccagtact | cctgccactt | ccactagctt | 2760 |
| gtttggctct | gcagctaaat | cgagtgtctc | tgcaagctct | ggaggggtgt | tcaacagtgc | 2820 |
| agctcctgct | gccccagcat | caactacaag | tagtgtgttt | ggcagtgtag | cctcttcaac | 2880 |
| aaacacttct | gcaaattctg | caaacatatt | tggaagctct | ggtggagcgg | ccactgctcc | 2940 |

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| | |
|--|------|
| tgggggctttt gtgtttggac agccagctag tactgctagc actgtttttg gaaactcgag | 3000 |
| cgaatcaaaa tcgacctttg ttttctctgg tcaggaaaat aaacccgtga cctctgcaag | 3060 |
| tacctctgtg actccatttc tatttggagc agtgtctgcc actactaccc cagcagctcc | 3120 |
| aagttttaac tttggacgaa caatcacttc aaatacaaca ggcactagct cgtctccatt | 3180 |
| tatctttggt gctggtgcaa gtggctctgc ttcttcaagt ataacggctc aggccaatcc | 3240 |
| agtgccagca tttgggcaaa gttctaatacc gtctactgca cccgcttttg gctcttcaac | 3300 |
| ttcagttcca gtgtttccag ctgggagttc tcagcaagtc ccggcctttg gttcgagtag | 3360 |
| tgacaaccc cctgtgtttg ggcaacaagc cgctcagcct tcttttggat ctctgtctgc | 3420 |
| accagtgct ggatctggtt tcccgttttg caacaacgca aacttcaact ttaacagcac | 3480 |
| aaattcatca ggtggagtct tcacgtttta tgcaaattca ggatccacca cccaaccacc | 3540 |
| tccccagga tacatgttta atgcagctgc gccaggtttt aacataggaa cgaatggcag | 3600 |
| gactactcca gcatctacta tttctactcg caagataaag accgccagaa gaagaaagta | 3660 |
| attgaatgaa tgtactggaa gtaatggttg tttcaagaaa tgaatggtgt ccctgcattg | 3720 |
| tgcaaatact ggagtgttcc tcatgctgtg tgtagtggaa gtcagatcag cccaaggaca | 3780 |
| aaaatatatg ctgaaacttg tctctttttc ctctgtaatt aaaacatggt gatgggaaat | 3840 |
| ttcttaacca agaaatctga ttccggcgcc tcctttgttt acctgacttg gcatgatttg | 3900 |
| gctatacgag tgtttatagc ctgcacagcg aatggctttt gtataatacc tctttcatct | 3960 |
| gcaccactat tttattgatg ctttgaaatt gtaattgtga gtgaggagcc gtgtataggt | 4020 |
| tacagactga tttctacacc acagttgtgc tggatgaatgt gtggagcgga gtgtagtgtg | 4080 |
| caccgaaact tttctgctta cggaagactg actcatgaat ggtccttaca taggatgtgc | 4140 |
| tagatctgta cttctctttc aaatatatgc cttttcttct ctttctctc cccctgttt | 4200 |
| tcattcagct cttgtcatct tctccattat tttattatat tcatgtaaat acatttgttt | 4260 |
| ctccatgtac ctttcagcat aaactaaatc aaaaaaaaaa aaaaa | 4305 |

<210> 6

<211> 1219

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 6

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Arg | Ser | Leu | Tyr | Ile | Lys | Pro | Ser | Leu | Thr | Pro | Ser | Ala | Val |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Asn | Thr | Asn | Ser | Arg | Arg | Ile | Gln | Pro | Asp | Lys | His | Asn | Glu | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |

Thr Lys Asn Asn Leu Gln Ser Thr Ser Gln Ser His Ser Phe Ser Tyr
35 40 45

Pro Lys Phe Ser Thr Pro Ala Ser Asn Gly Leu Ser Ser Gly Thr Gly
50 55 60

Gly Gly Lys Met Met Arg Glu Lys Gly Ser His Tyr Ser Thr Lys Pro
65 70 75 80

Ala Asn Glu Glu Leu Asp Gly Pro Val Leu Pro Glu Ile Pro Leu Pro
85 90 95

Leu Ser Thr Ala Ala Leu Pro Ser Phe Gln Phe Ser Thr Leu Ser Gly
100 105 110

Ser Ala Thr Ser Pro Ile Ser Val Thr Lys Pro Ala Asn Ser Thr Thr
115 120 125

Cys His Leu Thr Ser Ser Ser Pro Ser Phe Thr Phe Ser Ser Pro Ile
130 135 140

Val Lys Ser Thr Glu Ser Asn Ala Gln Phe Ser Gly Ser Ser Val Asp
145 150 155 160

Phe Thr Phe Ser Val Pro Ala Ala Lys Ala Ser Ser Ala Thr Ser Asp
165 170 175

Glu Ser Lys Val Ser Ala Val Ser Ser Ala Ala Lys Thr His Ala Ala
180 185 190

Val Asn Ser Ser Ala Lys Asn Thr Asp Asp Glu Gln Val Gly Phe Cys
195 200 205

Lys Pro Ala Lys Thr Leu Lys Glu Gly Ser Val Leu Asp Met Leu Arg
210 215 220

Ser Pro Gly Phe Ser Ser Leu Pro Ser Leu Leu Thr Ser Glu Ser Thr
225 230 235 240

Leu Asn Arg Ser Thr Pro Thr Leu Ser Lys Thr Val Gly Asn Thr Phe
245 250 255

Ser Pro Ala Asn Val Ser Leu Gly Val Gly Ser Lys Gln Phe Gly Leu
260 265 270

Trp Gln Cys Ser Ala Cys Phe His Glu Asn Met Ser Ser Asp Ser Asn
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Cys Ile Ser Cys Ser Ala Val Lys Pro Arg Pro Thr Glu Thr Ser Lys
290 295 300

Lys Leu Pro Ala Ser Pro Pro Ser Ser Asn Thr Lys Ser Thr Val Pro
305 310 315 320

Leu Ser Ser Thr Pro Gly Leu Gly Asp Ile Phe Lys Lys Pro Ala Gly
325 330 335

Met Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys Ala Glu Val Thr
340 345 350

Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr Cys Ile Lys Ala
355 360 365

Thr Leu Leu Ile Pro Ser Thr Thr Lys Ser Ile Asn Pro Ala Thr Asn
370 375 380

Thr Leu Ala Phe Ala Ser Cys Ser Ala Ser Ile Pro Asn Glu Glu Met
385 390 395 400

Phe Lys Lys Pro Met Gly Ser Trp Glu Cys Thr Val Cys His Met Gln
405 410 415

Asn Lys Thr Glu Asp Asn Thr Cys Val Gly Cys Lys Ala Glu Lys Pro
420 425 430

Gly Thr Val Lys Ser Val Pro Thr Ala Ala Pro Ser Gly Leu Leu Gly
435 440 445

Leu Leu His Gln Phe Lys Lys Pro Thr Gly Ser Trp Asp Cys Asp Val
450 455 460

Cys Leu Ile Gln Asn Lys Pro Glu Ala Ala Lys Cys Ile Ala Cys Glu
465 470 475 480

Ser Ala Lys Pro Gly Thr Lys Ala Glu Pro Lys Gly Thr Phe Asp Thr
485 490 495

Val Lys Asn Ser Val Ser Val Ala Pro Leu Ser Ser Gly Gln Leu Gly
500 505 510

Leu Leu Asp Gln Phe Lys Lys Ser Ala Gly Ser Trp Asp Cys Asp Val
515 520 525

Cys Leu Val Glu Asn Lys Pro Glu Ala Thr Lys Cys Val Ala Cys Glu
 530 535 540

Thr Ser Lys Pro Gly Thr Lys Ala Glu Leu Lys Gly Phe Gly Thr Ser
 545 550 555 560

Thr Phe Ser Ser Gly Thr Ala Ala Pro Thr Phe Lys Phe Gly Val Gln
 565 570 575

Ser Ser Asp Ser Thr Ala Glu Leu Lys Ser Gly Ala Ser Thr Ser Gly
 580 585 590

Phe Ala Lys Ser Ile Gly Asp Phe Lys Phe Gly Leu Val Ser Ala Ser
 595 600 605

Thr Thr Thr Glu Glu Thr Gly Lys Lys Ser Phe Thr Phe Gly Ser Ser
 610 615 620

Thr Thr Asn Glu Val Ser Ala Gly Phe Lys Phe Gly Ile Ala Gly Ser
 625 630 635 640

Ala Gln Thr Lys Pro Asp Thr Leu Ser Gln Ser Thr Thr Ser Gly Phe
 645 650 655

Thr Phe Gly Ser Val Ser Asn Thr Val Ser Leu Ala Pro Ala Ala Thr
 660 665 670

Ser Ser Ser Ser Thr Gly Leu Gln Val Ala Ala Ala Ile Ala Asp Ser
 675 680 685

Asn Leu Ala Thr Thr Ala Ala Leu Lys Ser Ala Glu Glu Lys Lys Ala
 690 695 700

Glu Ala Pro Thr Ile Thr Pro Phe Ser Phe Gly Lys Thr Asp Gln Asn
 705 710 715 720

Lys Glu Thr Ala Ser Thr Ser Phe Val Phe Gly Lys Lys Asp Glu Lys
 725 730 735

Thr Asp Ser Ala Pro Thr Gly Ser Ser Phe Ala Phe Gly Leu Lys Lys
 740 745 750

Asp Gly Glu Glu Ser Lys Pro Phe Leu Phe Gly Lys Pro Glu Pro Thr
 755 760 765

Lys Val Asp Gly Asn Ala Ala Ser Ala Gly Phe Ala Phe Gly Val Thr
 770 775 780

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Asn Pro Thr Glu Lys Lys Asp Ile Glu Gln Pro Gly Lys Ser Val Phe
785 790 795 800

Ala Phe Gly Ala Gln Thr Ser Ile Thr Asp Ala Gly Ala Ser Lys Gln
805 810 815

Pro Phe Ser Phe Leu Thr Asn Val Ser Ser Thr Ala Ala Ser Ser Ser
820 825 830

Thr Cys Gly Val Ser Ser Ser Val Phe Gly Ser Val Thr Gln Ser Ser
835 840 845

Thr Pro Ala Thr Pro Ser Asn Val Phe Gly Ser Ala Ile Ser Ala Asn
850 855 860

Ala Pro Ala Pro Ser Ser Gly Val Phe Gly Asn Leu Thr Pro Ser Asn
865 870 875 880

Ala Pro Ala Ala Ser Ser Thr Leu Phe Gly Asn Val Ala Pro Ser Ser
885 890 895

Thr Pro Ser Gly Ser Ser Gly Leu Phe Gly Thr Ala Ala Ala Ser Ser
900 905 910

Thr Pro Ala Thr Ser Thr Ser Leu Phe Gly Ser Ala Ala Lys Ser Ser
915 920 925

Ala Pro Ala Ser Ser Gly Gly Val Phe Asn Ser Ala Ala Pro Ala Ala
930 935 940

Pro Ala Ser Thr Thr Ser Ser Val Phe Gly Ser Val Ala Ser Ser Thr
945 950 955 960

Asn Thr Ser Ala Asn Ser Ala Asn Ile Phe Gly Ser Ser Gly Gly Ala
965 970 975

Ala Thr Ala Pro Gly Ala Phe Val Phe Gly Gln Pro Ala Ser Thr Ala
980 985 990

Ser Thr Val Phe Gly Asn Ser Ser Glu Ser Lys Ser Thr Phe Val Phe
995 1000 1005

Ser Gly Gln Glu Asn Lys Pro Val Thr Ser Ala Ser Thr Ser Val
1010 1015 1020

Thr Pro Phe Leu Phe Gly Ala Val Ser Ala Thr Thr Thr Pro Ala
1025 1030 1035

Ala Pro Ser Phe Asn Phe Gly Arg Thr Ile Thr Ser Asn Thr Thr
1040 1045 1050

Gly Thr Ser Ser Ser Pro Phe Ile Phe Gly Ala Gly Ala Ser Gly
1055 1060 1065

Ser Ala Ser Ser Ser Ile Thr Ala Gln Ala Asn Pro Val Pro Ala
1070 1075 1080

Phe Gly Gln Ser Ser Asn Pro Ser Thr Ala Pro Ala Phe Gly Ser
1085 1090 1095

Ser Thr Ser Val Pro Val Phe Pro Ala Gly Ser Ser Gln Gln Val
1100 1105 1110

Pro Ala Phe Gly Ser Ser Ser Ala Gln Pro Pro Val Phe Gly Gln
1115 1120 1125

Gln Ala Ala Gln Pro Ser Phe Gly Ser Pro Ala Ala Pro Ser Ala
1130 1135 1140

Gly Ser Gly Phe Pro Phe Gly Asn Asn Ala Asn Phe Asn Phe Asn
1145 1150 1155

Ser Thr Asn Ser Ser Gly Gly Val Phe Thr Phe Asn Ala Asn Ser
1160 1165 1170

Gly Ser Thr Thr Gln Pro Pro Pro Pro Gly Tyr Met Phe Asn Ala
1175 1180 1185

Ala Ala Pro Gly Phe Asn Ile Gly Thr Asn Gly Arg Thr Thr Pro
1190 1195 1200

Ala Ser Thr Ile Ser Thr Arg Lys Ile Lys Thr Ala Arg Arg Arg
1205 1210 1215

Lys

<210> 7

<211> 10697

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 7

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|--|------|
| cacagtgggc ctccgccggc tacggcgctg cgtcactggg ttgcaggcgc tttcctcttg | 60 |
| gaagtggcga ctgctgcggg cctgagcgct ggtctcacgc gcctcgggag ccagggttggc | 120 |
| ggcgcgatga ggcgcagcaa ggctgacgtg gagcggtaga tcgcctcggg gcagggctcc | 180 |
| accccgctgc ctcgacagaa gtcaatgaaa ggattctatt ttgcaaagct gtattatgaa | 240 |
| gctaaagaat atgatcttgc taaaaaatac atatgtactt acattaatgt gcaagagagg | 300 |
| gatcccaaag ctcacagatt tctgggtctt ctttatgaat tggaagaaaa cacagacaaa | 360 |
| gccgttgaat gttacaggcg ttcagtggaa ttaaaccaa cacaaaaaga tcttgtgttg | 420 |
| aagattgcag aattgctttg taaaaatgat gttactgatg gaagagcaaa atactggctt | 480 |
| gaaagagcag ccaaactttt cccaggaagt cctgcaattt ataaactaaa ggaacagctt | 540 |
| ctagatttg aaggtgaaga tggatggaat aaactttttg acttgattca gtcagaactt | 600 |
| tatgtaagac ctgatgacgt ccatgtgaac atccggctag tggaggtgta tcgctcaact | 660 |
| aaaagattga aggatgctgt ggcccactgc catgaggcag agaggaacat agctttgcgt | 720 |
| tcaagtttag aatggaattc gtgtgttgta cagaccctta aggaatatct ggagtcttta | 780 |
| cagtgtttgg agtctgataa aagtgaactgg cgagcaacca atacagactt actyctggcc | 840 |
| tatgctaate ttatgcttct tacgctttcc actagagatg tgcaggaaa tagagaatta | 900 |
| ctgcaaagtt ttgatagtgc tcttcagtct gtgaaatctt tgggtggaaa tgatgaactg | 960 |
| tcagctactt tcttagaaat gaaaggacat ttctacatgc atgctggttc tctgcttttg | 1020 |
| aagatggggtc agcatagtag taatgttcaa tggcgagctc tttctgagct ggctgcattg | 1080 |
| tgctatctca tagcatttca ggttccaaga ccaaagatta aattaataaa aggtgaagct | 1140 |
| ggacaaaatc tgctggaaat gatggcctgt gaccgactga gccaatcagg gcacatgttg | 1200 |
| ctaaacttaa gtcgtggcaa gcaagatttt ttaaaagaga ttgttgaaac ttttgccaac | 1260 |
| aaaagcgggc agtctgcatt atatgatgct ctgttttcta gtcagtcacc taaggataca | 1320 |
| tcttttcttg gtagcgatga tattggaaac attgatgtac gagaaccaga gcttgaagat | 1380 |
| ttgactagat acgatgttgg tgctattcga gcacataatg gtagtcttca gcaccttact | 1440 |
| tggcttggct tacagtggaa ttcattgcct gctttacctg gaatccgaaa atggctaaaa | 1500 |
| cagcttttcc atcatttgcc ccatgaaacc tcaaggcttg aaacaaatgc acctgaatca | 1560 |
| atatgtattt tagatcttga agtatttctc cttggagtag tatataccag ccacttacia | 1620 |
| ttaaaggaga aatgtaattc tcaccacagc tcctatcagc cgttatgcct gccccttcct | 1680 |
| gtgtgtaaac agctttgtac agaaagacaa aaatcttggt gggatgcggg ttgtactctg | 1740 |
| attcacagaa aagcagtacc tggaaacgta gcaaaattga gacttctagt tcagcatgaa | 1800 |
| ataaacactc taagagccca ggaaaaacat ggccttcaac ctgctctgct tgtacattgg | 1860 |
| gcagaatgcc ttcagaaaac gggcagcggg cttaattctt tttatgatca acgagaatac | 1920 |

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| | |
|--|------|
| atagggagaa gtgttcatta ttggaagaaa gttttgccat tgttgaagat aataaaaaag | 1980 |
| aagaacagta ttctgaacc tattgatcct ctgtttaaac attttcatag tgtagacatt | 2040 |
| caggcatcag aaattgttga atatgaagaa gacgcacaca taacttttgc tatattggat | 2100 |
| gcagtaaag gaaatataga agatgctgtg actgcttttg aatctataaa aagtgttgtt | 2160 |
| tcttattgga atcttgcact gatttttcac aggaaggcag aagacattga aaatgatgcc | 2220 |
| ctttctcctg aagaacaaga agaatgcaaa aattatctga gaaagaccag ggactaccta | 2280 |
| ataaagatta tagatgacag tgattcaaat ctttcagtgg tcaagaaatt gcctgtgccc | 2340 |
| ctggagtctg taaaagagat gcttaattca gtcattgcagg aactcgaaga ctatagtga | 2400 |
| ggaggtcctc tctataaaaa tgggttctttg cgaaatgcag attcagaaat aaaacattct | 2460 |
| acaccgtctc ctaccaaata ttcactatca ccaagtaaaa gttacaagta ttctcccaaa | 2520 |
| acaccacctc gatgggcaga agatcagaat tctttactga aaatgatttg ccaacaagta | 2580 |
| gaggccatta agaaagaaat gcaggagtgtg aaactaaata gcagtaactc agcatcccct | 2640 |
| catcgttggc ccacagagaa ttatggacca gactcgggtc ctgatggata tcaggggtca | 2700 |
| cagacatttc atggggctcc actaacagtt gcaactactg gcccttcagt atattatagt | 2760 |
| cagtcaccag catataattc ccagtatctt ctcagaccag cagctaattgt tactcccaca | 2820 |
| aagggcccag tctatggcat gaataggctt ccacccaac agcatattta tgcctatccg | 2880 |
| caacagatgc acacaccgcc agtgcaaagc tcattctgctt gtatgttctc tcaggagatg | 2940 |
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<211> 3208

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

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Gly Ser Thr Pro Ser Pro Arg Gln Lys Ser Met Lys Gly Phe Tyr Phe
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Ala Lys Leu Tyr Tyr Glu Ala Lys Glu Tyr Asp Leu Ala Lys Lys Tyr

35

40

45

Ile Cys Thr Tyr Ile Asn Val Gln Glu Arg Asp Pro Lys Ala His Arg
50 55 60

Phe Leu Gly Leu Leu Tyr Glu Leu Glu Glu Asn Thr Asp Lys Ala Val
65 70 75 80

Glu Cys Tyr Arg Arg Ser Val Glu Leu Asn Pro Thr Gln Lys Asp Leu
85 90 95

Val Leu Lys Ile Ala Glu Leu Leu Cys Lys Asn Asp Val Thr Asp Gly
100 105 110

Arg Ala Lys Tyr Trp Leu Glu Arg Ala Ala Lys Leu Phe Pro Gly Ser
115 120 125

Pro Ala Ile Tyr Lys Leu Lys Glu Gln Leu Leu Asp Cys Glu Gly Glu
130 135 140

Asp Gly Trp Asn Lys Leu Phe Asp Leu Ile Gln Ser Glu Leu Tyr Val
145 150 155 160

Arg Pro Asp Asp Val His Val Asn Ile Arg Leu Val Glu Val Tyr Arg
165 170 175

Ser Thr Lys Arg Leu Lys Asp Ala Val Ala His Cys His Glu Ala Glu
180 185 190

Arg Asn Ile Ala Leu Arg Ser Ser Leu Glu Trp Asn Ser Cys Val Val
195 200 205

Gln Thr Leu Lys Glu Tyr Leu Glu Ser Leu Gln Cys Leu Glu Ser Asp
210 215 220

Lys Ser Asp Trp Arg Ala Thr Asn Thr Asp Leu Leu Leu Ala Tyr Ala
225 230 235 240

Asn Leu Met Leu Leu Thr Leu Ser Thr Arg Asp Val Gln Glu Ser Arg
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Glu Leu Leu Gln Ser Phe Asp Ser Ala Leu Gln Ser Val Lys Ser Leu
260 265 270

Gly Gly Asn Asp Glu Leu Ser Ala Thr Phe Leu Glu Met Lys Gly His
275 280 285

Phe Tyr Met His Ala Gly Ser Leu Leu Leu Lys Met Gly Gln His Ser
 290 295 300

Ser Asn Val Gln Trp Arg Ala Leu Ser Glu Leu Ala Ala Leu Cys Tyr
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Leu Ile Ala Phe Gln Val Pro Arg Pro Lys Ile Lys Leu Ile Lys Gly
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Glu Ala Gly Gln Asn Leu Leu Glu Met Met Ala Cys Asp Arg Leu Ser
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Gln Ser Gly His Met Leu Leu Asn Leu Ser Arg Gly Lys Gln Asp Phe
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Leu Lys Glu Ile Val Glu Thr Phe Ala Asn Lys Ser Gly Gln Ser Ala
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Leu Tyr Asp Ala Leu Phe Ser Ser Gln Ser Pro Lys Asp Thr Ser Phe
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Leu Gly Ser Asp Asp Ile Gly Asn Ile Asp Val Arg Glu Pro Glu Leu
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Glu Asp Leu Thr Arg Tyr Asp Val Gly Ala Ile Arg Ala His Asn Gly
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Ser Leu Gln His Leu Thr Trp Leu Gly Leu Gln Trp Asn Ser Leu Pro
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Ala Leu Pro Gly Ile Arg Lys Trp Leu Lys Gln Leu Phe His His Leu
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Pro His Glu Thr Ser Arg Leu Glu Thr Asn Ala Pro Glu Ser Ile Cys
 465 470 475 480

Ile Leu Asp Leu Glu Val Phe Leu Leu Gly Val Val Tyr Thr Ser His
 485 490 495

Leu Gln Leu Lys Glu Lys Cys Asn Ser His His Ser Ser Tyr Gln Pro
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Leu Cys Leu Pro Leu Pro Val Cys Lys Gln Leu Cys Thr Glu Arg Gln
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Lys Ser Trp Trp Asp Ala Val Cys Thr Leu Ile His Arg Lys Ala Val
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Thr Leu Arg Ala Gln Glu Lys His Gly Leu Gln Pro Ala Leu Leu Val
565 570 575

His Trp Ala Glu Cys Leu Gln Lys Thr Gly Ser Gly Leu Asn Ser Phe
580 585 590

Tyr Asp Gln Arg Glu Tyr Ile Gly Arg Ser Val His Tyr Trp Lys Lys
595 600 605

Val Leu Pro Leu Leu Lys Ile Ile Lys Lys Lys Asn Ser Ile Pro Glu
610 615 620

Pro Ile Asp Pro Leu Phe Lys His Phe His Ser Val Asp Ile Gln Ala
625 630 635 640

Ser Glu Ile Val Glu Tyr Glu Glu Asp Ala His Ile Thr Phe Ala Ile
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Leu Asp Ala Val Asn Gly Asn Ile Glu Asp Ala Val Thr Ala Phe Glu
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Ser Ile Lys Ser Val Val Ser Tyr Trp Asn Leu Ala Leu Ile Phe His
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Arg Lys Ala Glu Asp Ile Glu Asn Asp Ala Leu Ser Pro Glu Glu Gln
690 695 700

Glu Glu Cys Lys Asn Tyr Leu Arg Lys Thr Arg Asp Tyr Leu Ile Lys
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Ile Ile Asp Asp Ser Asp Ser Asn Leu Ser Val Val Lys Lys Leu Pro
725 730 735

Val Pro Leu Glu Ser Val Lys Glu Met Leu Asn Ser Val Met Gln Glu
740 745 750

Leu Glu Asp Tyr Ser Glu Gly Gly Pro Leu Tyr Lys Asn Gly Ser Leu
755 760 765

Arg Asn Ala Asp Ser Glu Ile Lys His Ser Thr Pro Ser Pro Thr Lys
770 775 780

Tyr Ser Leu Ser Pro Ser Lys Ser Tyr Lys Tyr Ser Pro Lys Thr Pro
785 790 795 800

Pro Arg Trp Ala Glu Asp Gln Asn Ser Leu Leu Lys Met Ile Cys Gln
805 810 815

Gln Val Glu Ala Ile Lys Lys Glu Met Gln Glu Leu Lys Leu Asn Ser
820 825 830

Ser Asn Ser Ala Ser Pro His Arg Trp Pro Thr Glu Asn Tyr Gly Pro
835 840 845

Asp Ser Val Pro Asp Gly Tyr Gln Gly Ser Gln Thr Phe His Gly Ala
850 855 860

Pro Leu Thr Val Ala Thr Thr Gly Pro Ser Val Tyr Tyr Ser Gln Ser
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Pro Ala Tyr Asn Ser Gln Tyr Leu Leu Arg Pro Ala Ala Asn Val Thr
885 890 895

Pro Thr Lys Gly Pro Val Tyr Gly Met Asn Arg Leu Pro Pro Gln Gln
900 905 910

His Ile Tyr Ala Tyr Pro Gln Gln Met His Thr Pro Pro Val Gln Ser
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Ser Ser Ala Cys Met Phe Ser Gln Glu Met Tyr Gly Pro Pro Ala Leu
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Arg Phe Glu Ser Pro Ala Thr Gly Ile Leu Ser Pro Arg Gly Asp Asp
945 950 955 960

Tyr Phe Asn Tyr Asn Val Gln Gln Thr Ser Thr Asn Pro Pro Leu Pro
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Glu Pro Gly Tyr Phe Thr Lys Pro Pro Ile Ala Ala His Ala Ser Arg
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Ser Ala Glu Ser Lys Thr Ile Glu Phe Gly Lys Thr Asn Phe Val Gln
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Pro Met Pro Gly Glu Gly Leu Arg Pro Ser Leu Pro Thr Gln Ala
1010 1015 1020

His Thr Thr Gln Pro Thr Pro Phe Lys Phe Asn Ser Asn Phe Lys
1025 1030 1035

Ser Asn Asp Gly Asp Phe Thr Phe Ser Ser Pro Gln Val Val Thr
Page 30

1040

1045

1050

Gln Pro Pro Pro Ala Ala Tyr Ser Asn Ser Glu Ser Leu Leu Gly
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Leu Leu Thr Ser Asp Lys Pro Leu Gln Gly Asp Gly Tyr Ser Gly
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Ala Lys Pro Ile Pro Gly Gly Gln Thr Ile Gly Pro Arg Asn Thr
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| Ala | Cys | Gln | Asn | Pro | Asp | Lys | Pro | Ser | Pro | Ser | Thr | Ser | Val | Pro |
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| Ala | Pro | Ala | Ser | Phe | Lys | Phe | Gly | Thr | Ser | Glu | Thr | Ser | Lys | Ala |
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| Pro | Lys | Ser | Gly | Phe | Glu | Gly | Met | Phe | Thr | Lys | Lys | Glu | Gly | Gln |
| 1580 | | | | | | 1585 | | | | | 1590 | | | |
| Trp | Asp | Cys | Ser | Val | Cys | Leu | Val | Arg | Asn | Glu | Ala | Ser | Ala | Thr |
| 1595 | | | | | | 1600 | | | | | 1605 | | | |
| Lys | Cys | Ile | Ala | Cys | Gln | Asn | Pro | Gly | Lys | Gln | Asn | Gln | Thr | Thr |
| 1610 | | | | | | 1615 | | | | | 1620 | | | |
| Ser | Ala | Val | Ser | Thr | Pro | Ala | Ser | Ser | Glu | Thr | Ser | Lys | Ala | Pro |
| 1625 | | | | | | 1630 | | | | | 1635 | | | |
| Lys | Ser | Gly | Phe | Glu | Gly | Met | Phe | Thr | Lys | Lys | Glu | Gly | Gln | Trp |
| 1640 | | | | | | 1645 | | | | | 1650 | | | |
| Asp | Cys | Ser | Val | Cys | Leu | Val | Arg | Asn | Glu | Ala | Ser | Ala | Thr | Lys |
| 1655 | | | | | | 1660 | | | | | 1665 | | | |
| Cys | Ile | Ala | Cys | Gln | Asn | Pro | Gly | Lys | Gln | Asn | Gln | Thr | Thr | Ser |
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| Ser | Gly | Phe | Glu | Gly | Met | Phe | Thr | Lys | Lys | Glu | Gly | Gln | Trp | Asp |
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| Cys | Ser | Val | Cys | Leu | Val | Arg | Asn | Glu | Ala | Ser | Ala | Thr | Lys | Cys |
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| Ile | Ala | Cys | Gln | Cys | Pro | Ser | Lys | Gln | Asn | Gln | Thr | Thr | Ala | Ile |
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| Ser | Thr | Pro | Ala | Ser | Ser | Glu | Ile | Ser | Lys | Ala | Pro | Lys | Ser | Gly |
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Phe Glu Gly Met Phe Ile Arg Lys Gly Gln Trp Asp Cys Ser Val
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 Asp Ala Ser Lys Pro Thr His Lys Pro Ile Ala Glu Ala Pro Ser
 1790 1795 1800
 Ala Phe Thr Leu Gly Ser Glu Met Lys Leu His Asp Ser Ser Gly
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 Ser Gln Val Gly Thr Gly Phe Lys Ser Asn Phe Ser Glu Lys Ala
 1820 1825 1830
 Ser Lys Phe Gly Asn Thr Glu Gln Gly Phe Lys Phe Gly His Val
 1835 1840 1845
 Asp Gln Glu Asn Ser Pro Ser Phe Met Phe Gln Gly Ser Ser Asn
 1850 1855 1860
 Thr Glu Phe Lys Ser Thr Lys Glu Gly Phe Ser Ile Pro Val Ser
 1865 1870 1875
 Ala Asp Gly Phe Lys Phe Gly Ile Ser Glu Pro Gly Asn Gln Glu
 1880 1885 1890
 Lys Lys Ser Glu Lys Pro Leu Glu Asn Gly Thr Gly Phe Gln Ala
 1895 1900 1905
 Gln Asp Ile Ser Gly Gln Lys Asn Gly Arg Gly Val Ile Phe Gly
 1910 1915 1920
 Gln Thr Ser Ser Thr Phe Thr Phe Ala Asp Leu Ala Lys Ser Thr
 1925 1930 1935
 Ser Gly Glu Gly Phe Gln Phe Gly Lys Lys Asp Pro Asn Phe Lys
 1940 1945 1950
 Gly Phe Ser Gly Ala Gly Glu Lys Leu Phe Ser Ser Gln Tyr Gly
 1955 1960 1965
 Lys Met Ala Asn Lys Ala Asn Thr Ser Gly Asp Phe Glu Lys Asp
 1970 1975 1980
 Asp Asp Ala Tyr Lys Thr Glu Asp Ser Asp Asp Ile His Phe Glu

1985

| | | | | | | | | | | | | | | |
|------|-----|-----|-----|-----|-----|------|-----|-----|-----|-----|------|-----|-----|-----|
| Pro | Val | Val | Gln | Met | Pro | Glu | Lys | Val | Glu | Leu | Val | Thr | Gly | Glu |
| 2000 | | | | | | 2005 | | | | | 2010 | | | |
| Glu | Asp | Glu | Lys | Val | Leu | Tyr | Ser | Gln | Arg | Val | Lys | Leu | Phe | Arg |
| 2015 | | | | | | 2020 | | | | | 2025 | | | |
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| 2030 | | | | | | 2035 | | | | | 2040 | | | |
| Leu | Lys | Ile | Leu | Lys | Asn | Glu | Val | Asn | Gly | Lys | Leu | Arg | Met | Leu |
| 2045 | | | | | | 2050 | | | | | 2055 | | | |
| Met | Arg | Arg | Glu | Gln | Val | Leu | Lys | Val | Cys | Ala | Asn | His | Trp | Ile |
| 2060 | | | | | | 2065 | | | | | 2070 | | | |
| Thr | Thr | Thr | Met | Asn | Leu | Lys | Pro | Leu | Ser | Gly | Ser | Asp | Arg | Ala |
| 2075 | | | | | | 2080 | | | | | 2085 | | | |
| Trp | Met | Trp | Leu | Ala | Ser | Asp | Phe | Ser | Asp | Gly | Asp | Ala | Lys | Leu |
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| Glu | Gln | Leu | Ala | Ala | Lys | Phe | Lys | Thr | Pro | Glu | Leu | Ala | Glu | Glu |
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| Pro | Leu | Gln | Thr | Pro | His | Lys | Leu | Val | Asp | Thr | Gly | Arg | Ala | Ala |
| 2135 | | | | | | 2140 | | | | | 2145 | | | |
| Lys | Leu | Ile | Gln | Arg | Ala | Glu | Glu | Met | Lys | Ser | Gly | Leu | Lys | Asp |
| 2150 | | | | | | 2155 | | | | | 2160 | | | |
| Phe | Lys | Thr | Phe | Leu | Thr | Asn | Asp | Gln | Thr | Lys | Val | Thr | Glu | Glu |
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| Glu | Asn | Lys | Gly | Ser | Gly | Thr | Gly | Ala | Ala | Gly | Ala | Ser | Asp | Thr |
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Leu Gln Asn Tyr Asp Asn Lys Gln Val Arg Ile Val Met Arg Arg
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Ser Glu Thr Met Asp Lys Pro Val Asp Leu Ser Thr Arg Lys Glu
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Ser Ser Asn Ser Gly Asp Phe Ala Phe Gly Ser Lys Asp Lys Asn
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Phe Gln Trp Ala Asn Thr Gly Ala Ala Val Phe Gly Thr Gln Ser
2855 2860 2865

Val Gly Thr Gln Ser Ala Gly Lys Val Gly Glu Asp Glu Asp Gly
2870 2875 2880

Ser Asp Glu Glu Val Val His Asn Glu Asp Ile His Phe Glu Pro
2885 2890 2895

Ile Val Ser Leu Pro Glu Val Glu Val Lys Ser Gly Glu Glu Asp
2900 2905 2910

Glu Glu Ile Leu Phe Lys Glu Arg Ala Lys Leu Tyr Arg Trp Asp
2915 2920 2925

Arg Asp Val Ser Gln Trp Lys Glu Arg Gly Val Gly Asp Ile Lys
Page 38

2930

2935

2940

Ile Leu Trp His Thr Met Lys Asn Tyr Tyr Arg Ile Leu Met Arg
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Arg Asp Gln Val Phe Lys Val Cys Ala Asn His Val Ile Thr Lys
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Thr Met Glu Leu Lys Pro Leu Asn Val Ser Asn Asn Ala Leu Val
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Trp Thr Ala Ser Asp Tyr Ala Asp Gly Glu Ala Lys Val Glu Gln
 2990 2995 3000

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Lys Thr Phe Glu Glu Cys Gln Gln Asn Leu Met Lys Leu Gln Lys
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Gly His Val Ser Leu Ala Ala Glu Leu Ser Lys Glu Thr Asn Pro
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Asn Ser Ile Phe His Arg Val Ile Pro Asp Phe Val Cys Gln Gly
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Gly Asp Ile Thr Lys His Asp Gly Thr Gly Gly Gln Ser Ile Tyr
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Gly Asp Lys Phe Glu Asp Glu Asn Phe Asp Val Lys His Thr Gly
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Pro Gly Leu Leu Ser Met Ala Asn Gln Gly Gln Asn Thr Asn Asn
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Ser Gln Phe Val Ile Thr Leu Lys Lys Ala Glu His Leu Asp Phe
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Lys His Val Val Phe Gly Phe Val Lys Asp Gly Met Asp Thr Val
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Arg Ile Thr Ile Thr Glu Cys Gly Gln Ile
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<211> 4346

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

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Gly Gly Cys Gly Gly Cys Gly Gly Cys Gly Thr Ala Gly Gly Gly Ala
20 25 30

Gly Gly Cys Cys Gly Gly Gly Gly Cys Cys Gly Gly Gly Gly Cys Thr
35 40 45

Gly Ala Gly Gly Cys Cys Gly Cys Gly Gly Cys Cys Gly Gly Gly Thr
50 55 60

Cys Thr Gly Cys Gly Ala Gly Gly Cys Cys Cys Thr Thr Gly Gly Gly
65 70 75 80

Gly Cys Gly Gly Cys Ala Gly Gly Cys Gly Gly Cys Gly Gly Cys Gly
85 90 95

Gly Cys Cys Cys Gly Gly Gly Gly Cys Thr Cys Gly Ala Gly Cys Cys
100 105 110

Cys Gly Gly Ala Gly Gly Cys Ala Gly Gly Ala Gly Cys Ala Gly Cys
115 120 125

Cys Gly Cys Cys Ala Thr Gly Gly Cys Cys Gly Ala Gly Ala Gly Cys
130 135 140

Ala Thr Cys Ala Thr Ala Ala Thr Thr Cys Gly Thr Gly Thr Cys Cys
145 150 155 160

Ala Gly Thr Cys Cys Cys Cys Ala Gly Ala Thr Gly Gly Ala Gly Thr

Gly Ala Ala Gly Cys Gly Gly Ala Thr Cys Ala Cys Ala Gly Cys Ala
180 185 190

Ala Cys Ala Ala Ala Gly Ala Gly Ala Gly Ala Ala Ala Cys Ala Gly
195 200 205

Cys Ala Gly Cys Ala Ala Cys Ala Thr Thr Thr Thr Thr Gly Ala Ala
210 215 220

Ala Ala Ala Gly Gly Thr Thr Gly Cys Ala Ala Ala Gly Gly Ala Gly
225 230 235 240

Thr Thr Thr Gly Gly Cys Thr Thr Cys Cys Ala Ala Ala Ala Thr Ala
245 250 255

Ala Thr Gly Gly Cys Thr Thr Cys Thr Cys Gly Gly Thr Thr Thr Ala
260 265 270

Cys Ala Thr Cys Ala Ala Thr Ala Gly Ala Ala Ala Cys Ala Ala Gly
275 280 285

Ala Cys Thr Gly Gly Ala Gly Ala Gly Ala Thr Ala Ala Cys Ala Gly
290 295 300

Cys Cys Thr Cys Cys Thr Cys Cys Ala Ala Cys Ala Ala Ala Thr Cys
305 310 315 320

Cys Cys Thr Cys Ala Ala Cys Thr Thr Gly Cys Thr Ala Ala Ala Ala
325 330 335

Ala Thr Cys Ala Ala Gly Cys Ala Thr Gly Gly Cys Gly Ala Thr Thr
340 345 350

Thr Gly Thr Thr Gly Thr Thr Cys Cys Thr Gly Thr Thr Thr Cys Cys
355 360 365

Cys Thr Cys Gly Ala Gly Cys Cys Thr Thr Gly Cys Thr Gly Gly Gly
370 375 380

Cys Cys Cys Thr Cys Ala Thr Cys Thr Gly Ala Ala Ala Thr Gly Gly
385 390 395 400

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Gly Gly Gly Cys Thr Thr Cys Ala Ala Gly Thr Cys Thr Thr Thr
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 595 600 605

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Cys Ala Cys Gly Cys Cys Thr Ala Cys Ala Thr Cys Cys Gly Gly Ala
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675 680 685

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690 695 700

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705 710 715 720

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755 760 765

Ala Thr Cys Ala Cys Gly Cys Thr Gly Ala Ala Cys Ala Gly Ala Cys
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Ala Gly Ala Ala Gly Thr Ala Cys Ala Gly Gly Cys Ala Thr Gly Thr
785 790 795 800

Gly Gly Ala Cys Ala Ala Thr Ala Thr Cys Ala Thr Gly Thr Thr Thr
805 810 815

Gly Ala Gly Ala Ala Thr Cys Ala Cys Ala Cys Cys Gly Thr Cys Gly
820 825 830

Cys Thr Gly Ala Cys Cys Gly Cys Thr Thr Thr Cys Thr Thr Gly Ala
835 840 845

Cys Thr Thr Cys Thr Gly Gly Ala Gly Ala Ala Ala Gly Ala Cys Ala
850 855 860

Gly Gly Gly Ala Ala Cys Cys Ala Gly Cys Ala Ala Thr Thr Thr Gly
865 870 875 880

Gly Gly Thr Ala Cys Thr Thr Ala Thr Ala Cys Gly Gly Ala Cys Gly
885 890 895

Gly Thr Ala Cys Ala Cys Cys Gly Ala Gly Cys Ala Cys Ala Ala Ala
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Thr cys Ala Gly Gly Gly cys Thr Gly Ala Ala Gly Thr Gly Gly Cys
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980 985 990

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995 1000 1005

Gly cys Thr Gly Ala Ala Gly Thr Gly Gly Thr cys Gly Ala Thr
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1130 1135 1140

Thr cys Ala Gly Ala Ala Gly Ala Gly Thr Gly cys Ala Thr cys
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Ala cys Thr Gly cys Ala Gly Gly Ala Gly Ala cys Thr Thr cys
Page 44

1160

1165

1170

Cys Ala Gly Ala Ala Cys Ala Ala Gly Cys Ala Thr Cys Cys Cys
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 1190 1195 1200

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2115

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 2450 2455 2460

Gly Thr Gly Gly Gly Gly Ala Cys Gly Cys Ala Gly Thr Gly Gly
 2465 2470 2475

Cys Cys Cys Thr Gly Gly Ala Cys Ala Cys Gly Gly Cys Thr Cys
 2480 2485 2490

Cys Cys Cys Thr Cys Thr Gly Cys Ala Gly Gly Thr Cys Thr Gly
 2495 2500 2505

Cys Ala Gly Gly Thr Cys Gly Gly Thr Thr Thr Gly Cys Thr Gly
 2510 2515 2520

Cys Cys Thr Gly Cys Cys Cys Thr Cys Cys Thr Cys Cys Thr Cys
 2525 2530 2535

Thr Cys Ala Cys Cys Cys Gly Ala Thr Gly Thr Cys Cys Ala Gly
 2540 2545 2550

Gly Thr Gly Gly Gly Ala Thr Thr Thr Thr Ala Ala Ala Gly Thr
 2555 2560 2565

Cys Thr Gly Cys Ala Thr Thr Gly Gly Thr Thr Ala Thr Ala Ala
 2570 2575 2580

Cys Ala Ala Cys Ala Gly Thr Thr Ala Thr Cys Ala Gly Thr Ala
 2585 2590 2595
 Ala Thr Thr Cys Cys Thr Gly Cys Cys Cys Ala Gly Ala Ala Gly
 2600 2605 2610
 Ala Cys Thr Thr Thr Thr Ala Thr Thr Thr Ala Thr Thr Thr Thr
 2615 2620 2625
 Thr Thr Thr Thr Thr Ala Ala Gly Ala Thr Ala Ala Ala Ala Ala
 2630 2635 2640
 Cys Thr Gly Cys Ala Cys Ala Ala Ala Ala Gly Gly Gly Gly Ala
 2645 2650 2655
 Gly Thr Gly Ala Gly Ala Gly Ala Gly Ala Cys Thr Ala Gly Thr
 2660 2665 2670
 Thr Thr Cys Cys Ala Cys Ala Thr Cys Cys Thr Thr Cys Cys Cys
 2675 2680 2685
 Thr Cys Cys Thr Thr Thr Ala Gly Thr Gly Ala Ala Gly Cys Cys
 2690 2695 2700
 Cys Cys Cys Gly Ala Gly Gly Thr Thr Gly Thr Gly Thr Cys Cys
 2705 2710 2715
 Ala Gly Gly Gly Thr Gly Ala Thr Gly Ala Gly Thr Gly Thr Gly
 2720 2725 2730
 Gly Ala Cys Gly Gly Gly Gly Gly Cys Ala Cys Cys Ala Gly Thr
 2735 2740 2745
 Cys Ala Gly Thr Thr Cys Thr Cys Cys Cys Thr Thr Gly Ala Ala
 2750 2755 2760
 Gly Thr Ala Ala Ala Cys Cys Thr Cys Ala Gly Thr Gly Cys Cys
 2765 2770 2775
 Thr Gly Ala Gly Ala Cys Thr Thr Thr Thr Cys Thr Ala Cys Cys
 2780 2785 2790
 Ala Ala Gly Cys Cys Ala Cys Ala Cys Ala Gly Cys Thr Gly Cys
 2795 2800 2805
 Ala Gly Cys Ala Ala Cys Thr Gly Cys Ala Gly Ala Thr Ala Cys
 2810 2815 2820

Thr Gly Cys Gly Gly Gly Cys Thr Gly Ala Gly Cys Ala Gly Gly
 2825 2830 2835

Ala Gly Cys Ala Gly Thr Gly Gly Thr Gly Gly Cys Gly Cys Cys
 2840 2845 2850

Thr Gly Cys Cys Cys Thr Gly Ala Gly Gly Cys Thr Gly Cys Cys
 2855 2860 2865

Cys Thr Gly Cys Gly Ala Thr Gly Gly Cys Cys Thr Gly Gly Gly
 2870 2875 2880

Thr Gly Gly Gly Ala Gly Ala Gly Cys Thr Gly Gly Gly Thr Cys
 2885 2890 2895

Ala Cys Cys Gly Gly Thr Gly Cys Cys Gly Ala Thr Gly Cys Thr
 2900 2905 2910

Cys Thr Gly Gly Cys Cys Cys Thr Cys Cys Cys Cys Ala Ala Thr
 2915 2920 2925

Ala Cys Gly Cys Thr Gly Cys Thr Thr Cys Gly Thr Cys Cys Cys
 2930 2935 2940

Ala Cys Thr Gly Cys Ala Cys Cys Gly Cys Cys Thr Gly Gly Cys
 2945 2950 2955

Thr Gly Ala Gly Gly Gly Cys Gly Thr Thr Ala Gly Gly Gly
 2960 2965 2970

Cys Thr Gly Thr Gly Cys Cys Thr Cys Thr Thr Gly Thr Gly Ala
 2975 2980 2985

Gly Gly Gly Cys Cys Ala Thr Thr Thr Gly Gly Gly Ala Cys Cys
 2990 2995 3000

Thr Cys Cys Cys Thr Gly Gly Gly Gly Cys Ala Cys Thr Gly Cys
 3005 3010 3015

Ala Cys Ala Ala Thr Thr Gly Ala Thr Ala Gly Thr Gly Thr Ala
 3020 3025 3030

Cys Cys Ala Ala Thr Ala Gly Gly Gly Gly Ala Gly Ala Cys
 3035 3040 3045

Thr Gly Gly Gly Cys Gly Ala Thr Cys Thr Gly Gly Ala Ala Cys
 3050 3055 3060

3050

3055

3060

Ala Gly Cys Ala Cys Gly Thr Gly Gly Thr Gly Gly Gly Gly Thr
 3065 3070 3075

Cys Cys Thr Gly Cys Thr Thr Gly Thr Gly Thr Gly Cys Thr Cys
 3080 3085 3090

Thr Gly Cys Gly Thr Thr Cys Cys Thr Cys Thr Gly Thr Gly Gly
 3095 3100 3105

Cys Gly Thr Gly Gly Cys Cys Ala Gly Gly Cys Cys Gly Gly Gly
 3110 3115 3120

Gly Cys Cys Thr Gly Gly Cys Thr Cys Thr Thr Ala Cys Cys Cys
 3125 3130 3135

Gly Gly Gly Gly Ala Gly Thr Gly Gly Thr Gly Gly Gly Cys Ala
 3140 3145 3150

Thr Cys Thr Cys Gly Ala Thr Gly Cys Thr Thr Cys Thr Thr Thr
 3155 3160 3165

Gly Cys Cys Thr Thr Ala Ala Thr Gly Ala Thr Gly Gly Cys Cys
 3170 3175 3180

Ala Cys Ala Thr Cys Thr Gly Gly Gly Cys Thr Gly Cys Thr Cys
 3185 3190 3195

Thr Gly Cys Ala Cys Cys Cys Ala Cys Gly Gly Gly Ala Gly Ala
 3200 3205 3210

Gly Gly Cys Thr Gly Gly Cys Cys Cys Ala Gly Cys Thr Gly Cys
 3215 3220 3225

Ala Gly Ala Cys Thr Gly Cys Thr Thr Ala Gly Gly Gly Ala Cys
 3230 3235 3240

Thr Thr Cys Thr Gly Thr Gly Thr Cys Cys Ala Thr Cys Cys Thr
 3245 3250 3255

Gly Gly Gly Gly Gly Thr Ala Ala Gly Cys Cys Cys Ala Cys
 3260 3265 3270

Gly Thr Gly Ala Cys Cys Cys Ala Cys Ala Thr Thr Cys Thr Thr
 3275 3280 3285

Gly Gly Cys Ala Cys Thr Ala Thr Gly Ala Ala Cys Ala Gly Ala
 3290 3295 3300
 Gly Ala Ala Cys Ala Thr Thr Thr Gly Cys Cys Thr Gly Thr Thr
 3305 3310 3315
 Gly Gly Cys Thr Thr Cys Thr Gly Ala Ala Gly Thr Gly Gly Thr
 3320 3325 3330
 Cys Ala Gly Gly Gly Cys Cys Ala Thr Gly Gly Cys Thr Gly Ala
 3335 3340 3345
 Cys Ala Cys Cys Thr Cys Cys Ala Gly Gly Thr Cys Cys Gly Cys
 3350 3355 3360
 Cys Thr Gly Gly Cys Ala Thr Gly Gly Gly Ala Cys Ala Cys Cys
 3365 3370 3375
 Ala Ala Gly Thr Gly Gly Ala Ala Gly Gly Cys Cys Cys Ala Ala
 3380 3385 3390
 Gly Cys Ala Gly Cys Thr Cys Ala Thr Cys Thr Gly Cys Thr Cys
 3395 3400 3405
 Thr Thr Gly Gly Gly Ala Cys Cys Ala Gly Gly Gly Gly Cys Cys
 3410 3415 3420
 Ala Gly Thr Thr Gly Gly Gly Thr Thr Gly Gly Gly Thr Cys Thr
 3425 3430 3435
 Gly Gly Thr Cys Ala Cys Gly Gly Cys Ala Gly Ala Gly Cys Thr
 3440 3445 3450
 Thr Thr Thr Gly Thr Gly Gly Ala Gly Gly Gly Thr Cys Ala Gly
 3455 3460 3465
 Gly Ala Ala Gly Gly Gly Thr Gly Gly Ala Gly Ala Gly Gly Ala
 3470 3475 3480
 Gly Cys Thr Gly Gly Gly Thr Thr Gly Ala Ala Gly Cys Gly Gly
 3485 3490 3495
 Ala Cys Thr Gly Cys Thr Gly Cys Gly Gly Ala Thr Gly Cys Ala
 3500 3505 3510
 Ala Cys Thr Cys Cys Cys Ala Gly Cys Thr Thr Gly Cys Cys Cys
 3515 3520 3525

Ala Cys Cys Gly Cys Gly Gly Gly Cys Thr Gly Thr Cys Thr Gly
 3530 3535 3540
 Cys Thr Cys Thr Cys Cys Cys Thr Cys Cys Thr Ala Gly Cys Ala
 3545 3550 3555
 Gly Cys Thr Gly Thr Cys Ala Cys Ala Cys Thr Gly Ala Ala Gly
 3560 3565 3570
 Thr Thr Thr Thr Gly Thr Cys Cys Thr Cys Thr Gly Cys Thr Gly
 3575 3580 3585
 Thr Cys Thr Cys Cys Thr Cys Thr Gly Gly Thr Cys Cys Thr Gly
 3590 3595 3600
 Ala Gly Ala Thr Gly Ala Gly Cys Thr Gly Thr Gly Ala Gly Cys
 3605 3610 3615
 Cys Thr Ala Gly Gly Thr Gly Gly Cys Cys Ala Ala Gly Gly Cys
 3620 3625 3630
 Thr Thr Cys Cys Thr Gly Cys Ala Thr Thr Gly Cys Thr Thr Cys
 3635 3640 3645
 Cys Cys Thr Gly Thr Gly Ala Gly Thr Cys Cys Ala Ala Gly Gly
 3650 3655 3660
 Cys Cys Thr Thr Cys Cys Cys Cys Cys Ala Cys Cys Ala Cys Thr
 3665 3670 3675
 Gly Gly Gly Cys Ala Gly Ala Gly Gly Cys Thr Gly Gly Ala Cys
 3680 3685 3690
 Ala Gly Cys Ala Cys Gly Gly Ala Cys Thr Thr Cys Thr Ala Gly
 3695 3700 3705
 Ala Gly Ala Gly Ala Gly Cys Cys Gly Cys Gly Thr Thr Gly Cys
 3710 3715 3720
 Cys Ala Gly Thr Thr Cys Cys Thr Cys Thr Cys Cys Ala Cys
 3725 3730 3735
 Thr Cys Gly Cys Thr Cys Gly Thr Cys Cys Thr Thr Ala Thr Cys
 3740 3745 3750
 Cys Ala Cys Cys Ala Cys Gly Cys Thr Ala Thr Thr Ala Thr Ala
 3755 3760 3765

Gly Thr Thr Thr Cys Cys Gly Thr Thr Gly Thr Cys Cys Thr Cys
3770 3775 3780

Cys Ala Cys Cys Ala Gly Cys Ala Thr Thr Thr Cys Cys Cys Thr
3785 3790 3795

Thr Ala Cys Thr Cys Thr Gly Ala Ala Gly Thr Thr Cys Cys Gly
3800 3805 3810

Gly Cys Ala Thr Thr Cys Ala Cys Ala Thr Cys Ala Thr Thr Cys
3815 3820 3825

Ala Thr Gly Thr Thr Thr Thr Cys Thr Thr Thr Thr Gly Thr Cys
3830 3835 3840

Thr Thr Thr Thr Ala Gly Cys Thr Ala Ala Ala Gly Gly Ala Ala
3845 3850 3855

Ala Ala Gly Cys Ala Thr Thr Gly Gly Cys Gly Ala Thr Thr Thr
3860 3865 3870

Gly Thr Cys Thr Gly Ala Thr Thr Cys Thr Gly Gly Thr Thr Thr
3875 3880 3885

Thr Gly Ala Gly Thr Thr Ala Cys Thr Cys Thr Thr Thr Gly Thr
3890 3895 3900

Thr Cys Ala Gly Thr Ala Ala Thr Gly Cys Ala Cys Thr Thr Thr
3905 3910 3915

Ala Thr Thr Thr Thr Ala Thr Thr Gly Thr Cys Cys Ala Ala Ala
3920 3925 3930

Gly Ala Gly Ala Gly Thr Cys Ala Gly Ala Gly Cys Thr Ala Ala
3935 3940 3945

Gly Cys Ala Thr Ala Cys Ala Gly Gly Cys Thr Thr Gly Gly Gly
3950 3955 3960

Gly Gly Thr Gly Ala Gly Cys Cys Cys Thr Gly Cys Thr Gly Thr
3965 3970 3975

Gly Ala Gly Ala Gly Thr Thr Cys Ala Gly Gly Cys Cys Cys Thr
3980 3985 3990

Gly Gly Gly Ala Gly Gly Cys Thr Cys Ala Gly Cys Cys Ala Cys
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3995

Cys Thr Cys Cys Thr Cys Thr Thr Gly Thr Gly Gly Gly Ala Ala
4010 4015 4020

Gly Gly Ala Gly Gly Thr Cys Thr Cys Ala Gly Cys Cys Cys Cys
4025 4030 4035

Ala Cys Cys Thr Cys Gly Cys Ala Thr Cys Thr Thr Cys Ala Cys
4040 4045 4050

Cys Thr Gly Cys Cys Cys Thr Thr Gly Gly Thr Gly Thr Gly Gly
4055 4060 4065

Ala Cys Ala Cys Ala Cys Cys Thr Cys Thr Cys Ala Thr Gly
4070 4075 4080

Cys Thr Ala Cys Cys Ala Gly Cys Ala Cys Cys Ala Thr Ala Ala
4085 4090 4095

Thr Cys Cys Ala Gly Thr Gly Gly Gly Gly Thr Gly Ala Cys
4100 4105 4110

Thr Gly Gly Gly Thr Gly Cys Ala Cys Ala Cys Cys Thr Gly Cys
4115 4120 4125

Cys Cys Ala Gly Gly Thr Gly Ala Ala Cys Ala Cys Ala Gly Cys
4130 4135 4140

Gly Gly Cys Thr Gly Cys Cys Ala Gly Thr Cys Thr Cys Cys Thr
4145 4150 4155

Gly Gly Thr Cys Cys Cys Gly Ala Gly Ala Gly Gly Ala Gly Gly
4160 4165 4170

Thr Gly Gly Gly Gly Cys Cys Thr Gly Gly Cys Cys Cys Thr Gly
4175 4180 4185

Gly Cys Thr Cys Cys Cys Thr Cys Cys Ala Ala Cys Cys Ala Gly
4190 4195 4200

Cys Thr Gly Cys Thr Cys Cys Thr Gly Gly Gly Ala Cys Ala Cys
4205 4210 4215

Ala Gly Gly Thr Gly Cys Thr Cys Cys Thr Gly Cys Thr Thr Cys
4220 4225 4230

Gly Gly Cys Thr Cys Thr Gly Thr Thr Thr Cys Gly Gly Cys Thr
 4235 4240 4245

Cys Ala Cys Ala Gly Gly Thr Gly Thr Gly Cys Ala Thr Cys Ala
 4250 4255 4260

Cys Thr Gly Gly Gly Cys Thr Thr Gly Gly Ala Thr Thr Thr Gly
 4265 4270 4275

Cys Ala Thr Thr Ala Cys Ala Thr Thr Gly Ala Cys Cys Cys Cys
 4280 4285 4290

Ala Gly Cys Cys Cys Thr Gly Cys Ala Gly Thr Gly Gly Ala Ala
 4295 4300 4305

Cys Cys Thr Ala Ala Thr Ala Ala Ala Ala Gly Cys Gly Cys Cys
 4310 4315 4320

Thr Gly Ala Ala Gly Cys Ala Ala Ala Ala Ala Ala Ala Ala Ala
 4325 4330 4335

Ala Ala Ala Ala Ala Ala Ala Ala
 4340 4345

<210> 10

<211> 608

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 10

Met Ala Glu Ser Ile Ile Ile Arg Val Gln Ser Pro Asp Gly Val Lys
 1 5 10 15

Arg Ile Thr Ala Thr Lys Arg Glu Thr Ala Ala Thr Phe Leu Lys Lys
 20 25 30

Val Ala Lys Glu Phe Gly Phe Gln Asn Asn Gly Phe Ser Val Tyr Ile
 35 40 45

Asn Arg Asn Lys Thr Gly Glu Ile Thr Ala Ser Ser Asn Lys Ser Leu
 50 55 60

Asn Leu Leu Lys Ile Lys His Gly Asp Leu Leu Phe Leu Phe Pro Ser
 65 70 75 80

Ser Leu Ala Gly Pro Ser Ser Glu Met Glu Thr Ser Val Pro Pro Gly
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Phe Lys Val Phe Gly Ala Pro Asn Val Val Glu Asp Glu Ile Asp Gln
100 105 110

Tyr Leu Ser Lys Gln Asp Gly Lys Ile Tyr Arg Ser Arg Asp Pro Gln
115 120 125

Leu Cys Arg His Gly Pro Leu Gly Lys Cys Val His Cys Val Pro Leu
130 135 140

Glu Pro Phe Asp Glu Asp Tyr Leu Asn His Leu Glu Pro Pro Val Lys
145 150 155 160

His Met Ser Phe His Ala Tyr Ile Arg Lys Leu Thr Gly Gly Ala Asp
165 170 175

Lys Gly Lys Phe Val Ala Leu Glu Asn Ile Ser Cys Lys Ile Lys Ser
180 185 190

Gly Cys Glu Gly His Leu Pro Trp Pro Asn Gly Ile Cys Thr Lys Cys
195 200 205

Gln Pro Ser Ala Ile Thr Leu Asn Arg Gln Lys Tyr Arg His Val Asp
210 215 220

Asn Ile Met Phe Glu Asn His Thr Val Ala Asp Arg Phe Leu Asp Phe
225 230 235 240

Trp Arg Lys Thr Gly Asn Gln Gln Phe Gly Tyr Leu Tyr Gly Arg Tyr
245 250 255

Thr Glu His Lys Asp Ile Pro Leu Gly Ile Arg Ala Glu Val Ala Ala
260 265 270

Ile Tyr Glu Pro Pro Gln Ile Gly Thr Gln Asn Ser Leu Glu Leu Leu
275 280 285

Glu Asp Pro Lys Ala Glu Val Val Asp Glu Ile Ala Ala Lys Leu Gly
290 295 300

Leu Arg Lys Val Gly Trp Ile Phe Thr Asp Leu Val Ser Glu Asp Thr
305 310 315 320

Arg Lys Gly Thr Val Arg Tyr Ser Arg Asn Lys Asp Thr Tyr Phe Leu
325 330 335

Ser Ser Glu Glu Cys Ile Thr Ala Gly Asp Phe Gln Asn Lys His Pro
 340 345 350

Asn Met Cys Arg Leu Ser Pro Asp Gly His Phe Gly Ser Lys Phe Val
 355 360 365

Thr Ala Val Ala Thr Gly Gly Pro Asp Asn Gln Val His Phe Glu Gly
 370 375 380

Tyr Gln Val Ser Asn Gln Cys Met Ala Leu Val Arg Asp Glu Cys Leu
 385 390 395 400

Leu Pro Cys Lys Asp Ala Pro Glu Leu Gly Tyr Ala Lys Glu Ser Ser
 405 410 415

Ser Glu Gln Tyr Val Pro Asp Val Phe Tyr Lys Asp Val Asp Lys Phe
 420 425 430

Gly Asn Glu Ile Thr Gln Leu Ala Arg Pro Leu Pro Val Glu Tyr Leu
 435 440 445

Ile Ile Asp Ile Thr Thr Thr Phe Pro Lys Asp Pro Val Tyr Thr Phe
 450 455 460

Ser Ile Ser Gln Asn Pro Phe Pro Ile Glu Asn Arg Asp Val Leu Gly
 465 470 475 480

Glu Thr Gln Asp Phe His Ser Leu Ala Thr Tyr Leu Ser Gln Asn Thr
 485 490 495

Ser Ser Val Phe Leu Asp Thr Ile Ser Asp Phe His Leu Leu Leu Phe
 500 505 510

Leu Val Thr Asn Glu Val Met Pro Leu Gln Asp Ser Ile Ser Leu Leu
 515 520 525

Leu Glu Ala Val Arg Thr Arg Asn Glu Glu Leu Ala Gln Thr Trp Lys
 530 535 540

Arg Ser Glu Gln Trp Ala Thr Ile Glu Gln Leu Cys Ser Thr Val Gly
 545 550 555 560

Gly Gln Leu Pro Gly Leu His Glu Tyr Gly Ala Val Glu Gly Ser Thr
 565 570 575

His Thr Ala Thr Ala Ala Met Trp Ala Cys Gln His Cys Thr Phe Met
 580 585 590

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Asn Gln Pro Gly Thr Gly His Cys Glu Met Cys Ser Leu Pro Arg Thr
595 600 605

<210> 11
<211> 3067
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 11
ggtgggttta tctcaaggcc tgagtagccg gtaacaaacg agggttcccg ggattggacc 60
gacgcaccat gcctctgcca cttgatatca aaagaaagct aactgctaga tctgatcgag 120
ttaagagtgt ggatctgcat cctacagagc catggatgtt ggcaagtctt tacaatggca 180
gtgtgtgtgt ttggaatcat gaaacacaga cactggtgaa gacatttgaa gtatgtgatc 240
ttcctgttcg agctgcaaag tttgttgcaa ggaagaattg ggttgatgaca ggagcggatg 300
acatgcagat tagagtgttc aattacaata ctctggagag agttcatatg tttgaagcac 360
actcagacta cattcgctgt attgctgttc atccaacca gcctttcatt ctaactagca 420
gtgatgacat gcttattaag ctctgggact gggataaaaa atggctcttc tcacaagtgt 480
ttgaaggaca caccattat gttatgcaga ttgtgatcaa ccccaaagat aacaatcagt 540
ttgccagtgc ctctttggac aggactatca aggtgtggca gttgggctct tcgtcaccaa 600
acttcacttt ggaaggacat gagaaaggcg tgaattgcat tgattactac agtgggtggg 660
acaagccata cctcatttca ggtgcagatg accgtcttgt taaaatatgg gattatcaga 720
ataaaacatg tgtgcagaca ctggaaggac atgcccaaaa tgtgtcttgt gccagctttc 780
atcctgagtt gccaatcatt atcacagggt cagaagatgg aacagtacgt atttggcatt 840
caagcaccta ccggcttgag agcacactga attatggaat ggagagggta tgggtcgtgg 900
ccagtctaag agggtaaac aatgtcgctt tgggctatga tgaaggagc atcattgtta 960
agcttggctg ggaggaacct gccatgtcca tggatgccaa tggaaagata atttgggcca 1020
agcattcaga agtccagcag gccaacctaa aagcaatggg agatgctgaa attaaagatg 1080
gtgaaagatt gccactggca gtaaaggata tgggcagttg tgaaatatac cctcagacta 1140
ttcagcacia tcctaattgg cggtttgtgg tgggtgtgtg tgatggggag tatatcatct 1200
acacagcaat ggcattgaga aacaagagct ttggatctgc tcaggagttt gcatgggccc 1260
acgattcttc agagtatgca ataagagaga gcaacagcat tgtaaagata ttttaagaact 1320
ttaaggaaaa aaaatcattt aaaccagatt ttggagcaga aagtatctac ggcggcttct 1380
tattgggagt cagatctgta aatggcttag ccttctatga ctgggacaat acagaactca 1440
tacgaagaat tgaaattcag cccaaacata ttttctggtc tgactctgga gagctagtct 1500

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| | | | | | | |
|------------|-------------|------------|------------|------------|------------|------|
| gtattgctac | tgaggaatca | ttttttatcc | ttaagtatct | gtcagaaaaa | gtcttggtg | 1560 |
| cacaggaaac | acatgagggg | gttactgaag | atggcattga | agatgccttt | gaggttcttg | 1620 |
| gtgagattca | ggaaattgtg | aaaacagggc | tttgggtagg | cgattgcttc | atttacacaa | 1680 |
| gttctgtgaa | cagattaaat | tattatgttg | gaggagaaat | agtcaccatt | gcccacttgg | 1740 |
| acaggacgat | gtatctccta | ggctacattc | ctaaagacaa | caggctttat | ctgggggata | 1800 |
| aagaattgaa | catcattagc | tattccctgc | tggtttcagt | cctggaatac | cagacagctg | 1860 |
| tcatgcggag | ggacttttagc | atggctgata | aggtccttcc | taccattcca | aaagaacaga | 1920 |
| ggaccagagt | tgcacacttt | ttggaaaagc | agggcttcaa | gcagcaagct | cttacagtat | 1980 |
| ccacagatcc | tgagcatcgt | tttgagcttg | ctcttcagct | tggagagtta | aaaattgcat | 2040 |
| accagttagc | agtggaagca | gagtcagaac | agaagtggaa | acaacttgct | gaacttgcca | 2100 |
| ttagtaaatg | tcagtttggc | ctagcccagg | agtgcctgca | tcatgcacag | gattatgggg | 2160 |
| gcctgctgct | tttgccact | gcctctggaa | atgctaatat | ggtgaacaag | ctagcagagg | 2220 |
| gtgcgagag | agatggcaaa | aataatgtgg | cattcatgag | ctacttttta | cagggcaagg | 2280 |
| ttgatgcctg | cctagagctc | ttaattagaa | ctggacggct | gccagaagct | gccttcttgg | 2340 |
| cccgaactta | cttaccagct | caggtttcaa | gggtagtgaa | actctggaga | gagaatctct | 2400 |
| caaaagtcaa | tcagaaagca | gcagaatccc | ttgctgaccc | aacagagtat | gaaaacctgt | 2460 |
| tccctggatt | aaaagaagcc | tttgttgttg | aagaatgggt | gaaggaaaca | catgctgatc | 2520 |
| tgtggccagc | caaacaatac | ccacttgta | cgccaaatga | agagagaaat | gtcatggaag | 2580 |
| agggaaaaga | ctttcagccc | tcaagatcta | cagctcaaca | ggaacttgat | gggaaacctg | 2640 |
| cttctcctac | tccggttatt | gtggcctccc | acacagccaa | caaagaagaa | aagagtttac | 2700 |
| tcgaactaga | agtagatttg | gataatttgg | aattagaaga | tattgacaca | acagatatca | 2760 |
| atctggatga | agatattttg | gatgattgac | tgtaatgctt | tccatttacc | tgactaaaca | 2820 |
| gatcattatt | atatataggt | attgattgct | accctgacca | cagtgccttg | gactatgaga | 2880 |
| aacttcttag | atTTTTtat | gtaaatgctg | tggaccactg | ggagcacaat | gcccacatca | 2940 |
| tcttaagaag | agtttatgtg | cagcatttaa | atcactgtgt | tttccttggt | aactaaaaca | 3000 |
| gacatgggct | ttgatttttt | tcatactatt | agaccatatc | tcataaaacc | ttttgaatta | 3060 |
| aaaaaaa | | | | | | 3067 |

<210> 12

<211> 906

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 12

Met Pro Leu Arg Leu Asp Ile Lys Arg Lys Leu Thr Ala Arg Ser Asp
1 5 10 15

Arg Val Lys Ser Val Asp Leu His Pro Thr Glu Pro Trp Met Leu Ala
20 25 30

Ser Leu Tyr Asn Gly Ser Val Cys Val Trp Asn His Glu Thr Gln Thr
35 40 45

Leu Val Lys Thr Phe Glu Val Cys Asp Leu Pro Val Arg Ala Ala Lys
50 55 60

Phe Val Ala Arg Lys Asn Trp Val Val Thr Gly Ala Asp Asp Met Gln
65 70 75 80

Ile Arg Val Phe Asn Tyr Asn Thr Leu Glu Arg Val His Met Phe Glu
85 90 95

Ala His Ser Asp Tyr Ile Arg Cys Ile Ala Val His Pro Thr Gln Pro
100 105 110

Phe Ile Leu Thr Ser Ser Asp Asp Met Leu Ile Lys Leu Trp Asp Trp
115 120 125

Asp Lys Lys Trp Ser Cys Ser Gln Val Phe Glu Gly His Thr His Tyr
130 135 140

Val Met Gln Ile Val Ile Asn Pro Lys Asp Asn Asn Gln Phe Ala Ser
145 150 155 160

Ala Ser Leu Asp Arg Thr Ile Lys Val Trp Gln Leu Gly Ser Ser Ser
165 170 175

Pro Asn Phe Thr Leu Glu Gly His Glu Lys Gly Val Asn Cys Ile Asp
180 185 190

Tyr Tyr Ser Gly Gly Asp Lys Pro Tyr Leu Ile Ser Gly Ala Asp Asp
195 200 205

Arg Leu Val Lys Ile Trp Asp Tyr Gln Asn Lys Thr Cys Val Gln Thr
210 215 220

Leu Glu Gly His Ala Gln Asn Val Ser Cys Ala Ser Phe His Pro Glu
225 230 235 240

Leu Pro Ile Ile Ile Thr Gly Ser Glu Asp Gly Thr Val Arg Ile Trp
 245 250 255

His Ser Ser Thr Tyr Arg Leu Glu Ser Thr Leu Asn Tyr Gly Met Glu
 260 265 270

Arg Val Trp Cys Val Ala Ser Leu Arg Gly Ser Asn Asn Val Ala Leu
 275 280 285

Gly Tyr Asp Glu Gly Ser Ile Ile Val Lys Leu Gly Arg Glu Glu Pro
 290 295 300

Ala Met Ser Met Asp Ala Asn Gly Lys Ile Ile Trp Ala Lys His Ser
 305 310 315 320

Glu Val Gln Gln Ala Asn Leu Lys Ala Met Gly Asp Ala Glu Ile Lys
 325 330 335

Asp Gly Glu Arg Leu Pro Leu Ala Val Lys Asp Met Gly Ser Cys Glu
 340 345 350

Ile Tyr Pro Gln Thr Ile Gln His Asn Pro Asn Gly Arg Phe Val Val
 355 360 365

Val Cys Gly Asp Gly Glu Tyr Ile Ile Tyr Thr Ala Met Ala Leu Arg
 370 375 380

Asn Lys Ser Phe Gly Ser Ala Gln Glu Phe Ala Trp Ala His Asp Ser
 385 390 395 400

Ser Glu Tyr Ala Ile Arg Glu Ser Asn Ser Ile Val Lys Ile Phe Lys
 405 410 415

Asn Phe Lys Glu Lys Lys Ser Phe Lys Pro Asp Phe Gly Ala Glu Ser
 420 425 430

Ile Tyr Gly Gly Phe Leu Leu Gly Val Arg Ser Val Asn Gly Leu Ala
 435 440 445

Phe Tyr Asp Trp Asp Asn Thr Glu Leu Ile Arg Arg Ile Glu Ile Gln
 450 455 460

Pro Lys His Ile Phe Trp Ser Asp Ser Gly Glu Leu Val Cys Ile Ala
 465 470 475 480

Thr Glu Glu Ser Phe Phe Ile Leu Lys Tyr Leu Ser Glu Lys Val Leu
 485 490 495

Ala Ala Gln Glu Thr His Glu Gly Val Thr Glu Asp Gly Ile Glu Asp
500 505 510

Ala Phe Glu Val Leu Gly Glu Ile Gln Glu Ile Val Lys Thr Gly Leu
515 520 525

Trp Val Gly Asp Cys Phe Ile Tyr Thr Ser Ser Val Asn Arg Leu Asn
530 535 540

Tyr Tyr Val Gly Gly Glu Ile Val Thr Ile Ala His Leu Asp Arg Thr
545 550 555 560

Met Tyr Leu Leu Gly Tyr Ile Pro Lys Asp Asn Arg Leu Tyr Leu Gly
565 570 575

Asp Lys Glu Leu Asn Ile Ile Ser Tyr Ser Leu Leu Val Ser Val Leu
580 585 590

Glu Tyr Gln Thr Ala Val Met Arg Arg Asp Phe Ser Met Ala Asp Lys
595 600 605

Val Leu Pro Thr Ile Pro Lys Glu Gln Arg Thr Arg Val Ala His Phe
610 615 620

Leu Glu Lys Gln Gly Phe Lys Gln Gln Ala Leu Thr Val Ser Thr Asp
625 630 635 640

Pro Glu His Arg Phe Glu Leu Ala Leu Gln Leu Gly Glu Leu Lys Ile
645 650 655

Ala Tyr Gln Leu Ala Val Glu Ala Glu Ser Glu Gln Lys Trp Lys Gln
660 665 670

Leu Ala Glu Leu Ala Ile Ser Lys Cys Gln Phe Gly Leu Ala Gln Glu
675 680 685

Cys Leu His His Ala Gln Asp Tyr Gly Gly Leu Leu Leu Ala Thr
690 695 700

Ala Ser Gly Asn Ala Asn Met Val Asn Lys Leu Ala Glu Gly Ala Glu
705 710 715 720

Arg Asp Gly Lys Asn Asn Val Ala Phe Met Ser Tyr Phe Leu Gln Gly
725 730 735

Lys Val Asp Ala Cys Leu Glu Leu Leu Ile Arg Thr Gly Arg Leu Pro
740 745 750

Glu Ala Ala Phe Leu Ala Arg Thr Tyr Leu Pro Ser Gln Val Ser Arg
755 760 765

Val Val Lys Leu Trp Arg Glu Asn Leu Ser Lys Val Asn Gln Lys Ala
770 775 780

Ala Glu Ser Leu Ala Asp Pro Thr Glu Tyr Glu Asn Leu Phe Pro Gly
785 790 795 800

Leu Lys Glu Ala Phe Val Val Glu Glu Trp Val Lys Glu Thr His Ala
805 810 815

Asp Leu Trp Pro Ala Lys Gln Tyr Pro Leu Val Thr Pro Asn Glu Glu
820 825 830

Arg Asn Val Met Glu Glu Gly Lys Asp Phe Gln Pro Ser Arg Ser Thr
835 840 845

Ala Gln Gln Glu Leu Asp Gly Lys Pro Ala Ser Pro Thr Pro Val Ile
850 855 860

Val Ala Ser His Thr Ala Asn Lys Glu Glu Lys Ser Leu Leu Glu Leu
865 870 875 880

Glu Val Asp Leu Asp Asn Leu Glu Leu Glu Asp Ile Asp Thr Thr Asp
885 890 895

Ile Asn Leu Asp Glu Asp Ile Leu Asp Asp
900 905

<210> 13

<211> 914

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 13

Gly Gly Cys Gly Gly Cys Gly Ala Gly Cys Gly Gly Ala Ala Thr Gly
1 5 10 15

Cys Ala Gly Cys Gly Gly Cys Cys Cys Gly Ala Gly Gly Cys Cys Thr
20 25 30

Gly Gly Cys Cys Ala Cys Gly Thr Cys Cys Gly Cys Ala Cys Cys Cys
35 40 45

Gly Gly Gly Gly Gly Ala Gly Gly Gly Gly Gly Cys Cys Gly Cys Gly
50 55 60

Gly Cys Gly Gly Cys Cys Cys Ala Gly Gly Cys Cys Gly Gly Gly Gly
65 70 75 80

Gly Cys Cys Cys Gly Gly Cys Gly Cys Cys Gly Cys Cys Thr Gly Cys
85 90 95

Thr Cys Gly Ala Gly Cys Cys Gly Gly Gly Gly Ala Gly Cys Cys Cys
100 105 110

Thr Cys Gly Gly Gly Gly Cys Thr Gly Cys Gly Gly Thr Thr Gly Cys
115 120 125

Ala Gly Gly Ala Ala Cys Cys Thr Thr Cys Cys Cys Thr Cys Thr Ala
130 135 140

Cys Ala Cys Cys Ala Thr Cys Ala Ala Gly Gly Cys Thr Gly Thr Thr
145 150 155 160

Thr Thr Cys Ala Thr Cys Cys Thr Ala Gly Ala Thr Ala Ala Thr Gly
165 170 175

Ala Cys Gly Gly Gly Cys Gly Cys Cys Gly Gly Cys Thr Gly Cys Thr
180 185 190

Gly Gly Cys Cys Ala Ala Gly Thr Ala Thr Thr Ala Thr Gly Ala Thr
195 200 205

Gly Ala Cys Ala Cys Ala Thr Thr Cys Cys Cys Cys Thr Cys Cys Ala
210 215 220

Thr Gly Ala Ala Gly Gly Ala Gly Cys Ala Gly Ala Thr Gly Gly Thr
225 230 235 240

Thr Thr Thr Cys Gly Ala Gly Ala Ala Ala Ala Thr Gly Thr Cys
245 250 255

Thr Thr Cys Ala Ala Cys Ala Ala Gly Ala Cys Cys Ala Gly Cys Cys
260 265 270

Gly Gly Ala Cys Thr Gly Ala Gly Ala Gly Thr Gly Ala Gly Ala Thr
275 280 285

Thr Gly Cys Ala Thr Thr Thr Thr Thr Gly Gly Gly Gly Gly Thr
290 295 300

Ala Thr Gly Ala Cys Cys Ala Thr Cys Gly Thr Cys Thr Ala Cys Ala
305 310 315 320

Ala Gly Ala Ala Cys Ala Gly Cys Ala Thr Thr Gly Ala Cys Cys Thr
325 330 335

Cys Thr Thr Cys Cys Thr Ala Thr Ala Cys Gly Thr Gly Gly Thr Gly
340 345 350

Gly Gly Cys Thr Cys Ala Thr Cys Cys Thr Ala Cys Gly Ala Gly Ala
355 360 365

Ala Thr Gly Ala Gly Cys Thr Gly Ala Thr Gly Cys Thr Cys Ala Thr
370 375 380

Gly Thr Cys Thr Gly Thr Thr Cys Thr Cys Ala Cys Cys Thr Gly Cys
385 390 395 400

Cys Thr Gly Thr Thr Thr Gly Ala Gly Thr Cys Thr Cys Thr Gly Ala
405 410 415

Ala Cys Cys Ala Cys Ala Thr Gly Thr Thr Ala Ala Gly Gly Ala Ala
420 425 430

Gly Ala Ala Cys Gly Thr Gly Gly Ala Gly Ala Ala Gly Cys Gly Cys
435 440 445

Thr Gly Gly Thr Thr Gly Cys Thr Gly Gly Ala Gly Ala Ala Cys Ala
450 455 460

Thr Gly Gly Ala Cys Gly Gly Ala Gly Cys Cys Thr Thr Cys Thr Thr
465 470 475 480

Gly Gly Thr Gly Cys Thr Gly Gly Ala Cys Gly Ala Gly Ala Thr Thr
485 490 495

Gly Thr Gly Gly Ala Thr Gly Gly Cys Gly Gly Thr Gly Thr Gly Ala
500 505 510

Thr Thr Cys Thr Gly Gly Ala Gly Ala Gly Thr Gly Ala Cys Cys Cys
515 520 525

Cys Cys Ala Gly Cys Ala Ala Gly Thr Gly Ala Thr Cys Cys Ala Gly
530 535 540

Ala Ala Gly Gly Thr Gly Ala Ala Thr Thr Thr Thr Ala Gly Gly Gly
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545

cys Ala Gly Ala Thr Gly Ala Thr Gly Gly cys Gly Gly cys Thr Thr
565 570 575

Gly Ala Cys Thr Gly Ala Ala Cys Ala Gly Ala Gly Thr Gly Thr Gly
580 585 590

Gly Cys Cys Cys Ala Gly Gly Thr Thr Cys Thr Thr Cys Ala Gly Thr
595 600 605

cys Thr Gly Cys Cys Ala Ala Gly Gly Ala Ala cys Ala Ala Ala Thr
610 615 620

Thr Ala Ala Ala Thr Gly Gly Thr Cys Gly Thr Thr Ala Thr Thr Gly
625 630 635 640

Ala Ala Ala Thr Gly Ala Ala Gly Gly cys Thr Gly Thr Gly Gly Ala
645 650 655

Thr Thr Cys Ala Ala Gly Gly Cys Thr Cys Cys Cys Thr Gly Cys Cys
660 665 670

Cys Cys Cys Cys Ala Gly Ala Cys Cys Ala Thr Thr Thr Cys Cys Cys
675 680 685

Cys Ala Ala Thr cys cys Thr Gly Gly cys Ala Ala Ala Ala Gly cys
690 695 700

cys cys Ala Ala Ala Gly Ala Thr Cys cys cys Ala Gly Gly Gly Thr
705 710 715 720

cys Ala Gly Gly Ala Gly Ala Gly Ala cys Cys Cys Cys Thr cys Thr
725 730 735

Gly Thr Ala Thr cys cys cys cys Ala Gly Gly Thr cys cys cys Thr
740 745 750

cys cys cys Ala Gly Ala Ala cys Thr Gly Ala cys Thr cys cys Thr
755 760 765

Ala Ala Gly Gly Thr cys Thr cys cys Ala Gly cys cys Ala Gly Gly
770 775 780

Gly cys Thr Thr cys Thr Gly Ala Gly Ala Thr Gly cys Ala Ala Ala
785 790 795 800

Gly Gly Thr Thr Thr Gly Gly Cys Cys Thr Cys Ala Gly Gly Ala Gly
805 810 815

Ala Gly Thr Cys Ala Cys Cys Thr Thr Thr Cys Thr Cys Ala Cys
820 825 830

Gly Gly Cys Cys Cys Thr Gly Gly Cys Cys Thr Thr Ala Ala Cys Thr
835 840 845

Cys Ala Thr Ala Thr Cys Thr Thr Ala Gly Gly Cys Ala Thr Thr Cys
850 855 860

Cys Thr Gly Gly Cys Cys Cys Cys Ala Gly Gly Gly Cys Cys Cys Thr
865 870 875 880

Ala Ala Thr Ala Ala Ala Cys Cys Thr Gly Cys Thr Thr Thr Thr Gly
885 890 895

Thr Cys Thr Thr Cys Thr Gly Cys Ala Ala Ala Ala Ala Ala Ala
900 905 910

Ala Ala

<210> 14

<211> 210

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 14

Met Gln Arg Pro Glu Ala Trp Pro Arg Pro His Pro Gly Glu Gly Ala
1 5 10 15

Ala Ala Ala Gln Ala Gly Gly Pro Ala Pro Pro Ala Arg Ala Gly Glu
20 25 30

Pro Ser Gly Leu Arg Leu Gln Glu Pro Ser Leu Tyr Thr Ile Lys Ala
35 40 45

Val Phe Ile Leu Asp Asn Asp Gly Arg Arg Leu Leu Ala Lys Tyr Tyr
50 55 60

Asp Asp Thr Phe Pro Ser Met Lys Glu Gln Met Val Phe Glu Lys Asn
65 70 75 80

Val Phe Asn Lys Thr Ser Arg Thr Glu Ser Glu Ile Ala Phe Phe Gly
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Gly Met Thr Ile Val Tyr Lys Asn Ser Ile Asp Leu Phe Leu Tyr Val
100 105 110

Val Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ser Val Leu Thr
115 120 125

Cys Leu Phe Glu Ser Leu Asn His Met Leu Arg Lys Asn Val Glu Lys
130 135 140

Arg Trp Leu Leu Glu Asn Met Asp Gly Ala Phe Leu Val Leu Asp Glu
145 150 155 160

Ile Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Ile
165 170 175

Gln Lys Val Asn Phe Arg Ala Asp Asp Gly Gly Leu Thr Glu Gln Ser
180 185 190

Val Ala Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu
195 200 205

Leu Lys
210

<210> 15
<211> 5064
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 15
gagaagggga ccttcaggtc caggcaaagg gggaacttct gtcgtgggaa cgaaaaagaa 60
agaggattta caggggtggg ggacagaggg gcagcaggaa ccagaaggga gacagtggcg 120
gtcgcaccgg ggccgatccg agagttcccc ttagagaacg gagctcacgg gcggggagggc 180
ctcacctgct agtaggacgc agaaagacag aaggcgaagg agaccccctg ccgtagccat 240
cttgccctctc tgctgagcgg aagccccgt tcggctcctg tctgttagcg gcctctctag 300
gctaccactg acaccgtctc tgtggcccgg agcctaagag accggaagtt cgtgtttcca 360
ggcgcttccg gaaaccgcgg gagagggtcg ctgacgtgga ggcgtccgaa gggcagcagg 420
gtgtgtcggg gctcggatta agacatcgga gtcggagacc tgagagatgt taaccaaatt 480
cgagaccaag agcgcgcggg tcaaagggtc cagctttcac cccaaaagac cttggatcct 540
gactagttta cataatggg tcatccagtt atgggactat cggatgtgca ctctcattga 600

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| | |
|--|------|
| caagtttgat gaacatgatg gtccagtgcg aggcattgac ttccataagc agcagccact | 660 |
| gttcgtctct ggaggagatg actataagat taaggtttgg aattacaagc ttcggcgctg | 720 |
| tcttttcaca ttgcttgggc acttagatta tattcgcacc acgttttttc atcatgaata | 780 |
| tccctggatt ctgagtgcct ccgatgatca gaccatccga gtgtggaatt ggcaatctag | 840 |
| aacctgtggt tgtgtgttaa cagggcacaa ccattatgtg atgtgtgctc agttccaccc | 900 |
| cacagaagac ttggtagatc cagccagcct ggaccagact gtgcgcgttt gggatatttc | 960 |
| tggctcgagg aaaaaaac tgtcccctgg tgcggtggaa tcggatgtga gaggaataac | 1020 |
| tggggttgat ctatttggaa ctacagatgc agtgggtgaag catgtactag agggtcacga | 1080 |
| tcgtggagta aactgggctg ccttccaccc cactatgccc cttattgtat ctggggcaga | 1140 |
| tgatcgtaa gtgaagatct ggcgcatgaa tgaatcaaag gcatgggagg ttgataacctg | 1200 |
| ccggggccat tacaacaatg tatcttgtgc cgtcttccac cctcgccaag agttgatcct | 1260 |
| cagcaattct gaggacaaga gtattcgagt ctgggatatg tctaagcgga ctggggttca | 1320 |
| gactttccgc agagaccatg atcgtttctg ggtcctagct gctcaccta acctaacct | 1380 |
| ctttgcagca ggccatgatg gtggtatgat tgtgtttaag ctggaacggg aacggccagc | 1440 |
| ctatgctggt catggcaata tgctacacta tgtcaaggac cgattcttac gacagctgga | 1500 |
| tttcaacagc tccaaagatg tagctgtgat gcagttgcgg agtggttcca agtttccagt | 1560 |
| attcaatatg tcatacaatc cagcagaaaa tgcagtcctg ctttgtacaa gagctagcaa | 1620 |
| tctagagaat agtacctatg acctgtacac catccctaaa gatgctgact cccagaatcc | 1680 |
| tgatgcgcct gaagggaaac gatcctcagg cctgacagcc gtttgggtcg ctcgaaatcg | 1740 |
| gtttgctgtc ctagatcgga tgcattcgct tctgatcaag aatctgaaga atgagatcac | 1800 |
| caaaaaggta caggtgccca actgtgatga gatcttctat gctggcacag gcaatctcct | 1860 |
| gcttcgagat gcggactcta tcacactctt tgacgtacag cagaagcgga ctctggcatc | 1920 |
| tgtgaagatt tctaaagtga aatacgttat ctggtcagca gacatgtcac atgtagcact | 1980 |
| actagccaaa cacgccattg tgatctgtaa ccgcaaactg gatgctttat gtaacattca | 2040 |
| tgagaacatt cgtgtcaaga gtggggcctg ggatgagagt ggggtattta tctataccac | 2100 |
| aagcaaccac atcaaatatg ctgtcaccac tggggaccac gggatcattc gaactctgga | 2160 |
| tttaccatc tatgtcacac ggggtgaagg caacaatgta tactgcctag acagggagtg | 2220 |
| tcgtccccgg gtactacca ttgatccac tgagttcaaa ttcaagctgg ccctgatcaa | 2280 |
| cagaaaatat gatgaggtac tgcacatggt gaggaatgcc aaactagttg gccagtctat | 2340 |
| tattgcttat ctccagaaga agggctatcc tgaagtggca ctgcattttg tcaaggatga | 2400 |
| gaaaactcgc tttagtctgg cactggagtg tggaaacatt gagattgctc tggaagcagc | 2460 |

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| | |
|--|------|
| caaagcactg gatgacaaga actgctggga aaagctggga gaagtggccc tgctgcaggg | 2520 |
| gaaccaccag attgtggaaa tgtgctatca gcgtaccaa aactttgaca aagtttcctt | 2580 |
| cctgtatctt atcactggca acttagaaaa acttcgcaag atgatgaaga ttgctgagat | 2640 |
| cagaaaggac atgagtggcc actatcagaa tgccctatac ctgggtgatg tgtcagagcg | 2700 |
| tgtgcggatc ctgaagaact gtggacagaa gtccctggcc tatctcacag ctgctacca | 2760 |
| tggcttagat gaagaagctg agagcctaaa ggagacattt gaccagaga aggagacaat | 2820 |
| cccagacatt gaccctaag ccaagctgct ccagccacct gcacctatca tgccattgga | 2880 |
| taccaattgg cctttattga ctgtatcaa aggatttttt gaaggcacca ttgccagcaa | 2940 |
| aggggaagga ggagcactgg ctgctgacat tgacattgac actgttggtg cagagggctg | 3000 |
| gggagaggat gcagagctgc agttggatga agatggggtt gtggaggcta cagaagggtt | 3060 |
| gggggatgat gctcttggca agggacagga agaaggaggt ggctgggatg tagaagaaga | 3120 |
| tctggagctc cctcctgagc tggatatatc ccctggggca gctgggtggg ctgaagatgg | 3180 |
| tttctttgtg cccccaacca agggaacaag tccaactcag atctggtgta ataactctca | 3240 |
| gcttccagtt gatcacatcc tggcaggctc tttcgaaaca gccatgcggc tccttcatga | 3300 |
| ccaagtaggg gtaatccagt ttggccccta caagcaactg ttcctacaga catacgcccg | 3360 |
| aggccgcaca acctatcagg ctctgccctg cctaccctcc atgtatggct atcctaatcg | 3420 |
| caactggaag gatgcagggc tgaagaatgg tgtaccagct gtgggcctga agcttaatga | 3480 |
| cctcatccaa cggttgagc tgtgctacca gctcaccaca gttggcaaat ttgaggaggc | 3540 |
| tgtggaaaaa ttccgttcca tccttctcag tgtgccactt cttgttgtgg acaataaaca | 3600 |
| agagattgca gaggcccagc agctcatcac catttgccgt gagtacattg tgggtttgtc | 3660 |
| cgtaggagaca gaaaggaaga agctgcccga agagactcta gaacagcaga agcgcatctg | 3720 |
| tgagatggca gcctatttca cccactcaaa cctgcagcct gtgcacatga tcctggtgct | 3780 |
| gcgtacagcc ctcaatctgt tcttcaagct caagaacttc aagacagctg ccacctttgc | 3840 |
| tcggcgcccta ctagaactcg ggcccaagcc tgaggtggcc caacagaccc gaaaaatcct | 3900 |
| gtctgcctgt gagaagaatc ccacagatgc ctaccagctc aattatgaca tgcacaaccc | 3960 |
| ctttgacatt tgtgctgcat catatcgcc catctaccgt ggaaagccag tagaaaagtg | 4020 |
| tccactcagt ggggcctgct attcccctga gttcaaaggt caaatctgca gggtcaccac | 4080 |
| agtgacagag attggcaaag atgtgattgg ttttaaggatc agtcctctgc agtttcgcta | 4140 |
| aggccccctt tgtgtgcatg ggtcagtcac catatgttcc cccagagaa tgtgtctata | 4200 |
| tcctccttct aacagcacct tccccctgca gctactcttc agatctggct ctctgtaccc | 4260 |
| taaaacctag tatctttttc tcttctatgg aaaatccgaa ggtctaaact tgactttttt | 4320 |
| gaggtcttct caacttgact acagttgtgc tcataattgt ccttgccctt ccagcttaat | 4380 |

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ccaacatggc aacaccccgt ctctaataaa aatataaaaa ttagcctggc atggttagcat 4560
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tggtggttgc attcaactga gatcatacca cttcattcca gcctgggtga cagagcaaga 4680
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cctgtcaact agaaaggagc aggatgtaat aaatacattt tgggtgtgact aggccacacc 4860
aactcttaat catctcccat tttccttaga catttaaatt tcaaggcagg taccctctgt 4920
gtactcagaa atttgaagaa gttatttggg tttccaaaat gcacactgcg gggtattgat 4980
ttgttcttta caactattgt tctcatattt ctcacactaa ataaatctct atgagagctt 5040
cttgaaaaaa aaaaaaaaaa agcg 5064
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<210> 16
 <211> 1224
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct
 <400> 16

Met Leu Thr Lys Phe Glu Thr Lys Ser Ala Arg Val Lys Gly Leu Ser
 1 5 10 15

Phe His Pro Lys Arg Pro Trp Ile Leu Thr Ser Leu His Asn Gly Val
 20 25 30

Ile Gln Leu Trp Asp Tyr Arg Met Cys Thr Leu Ile Asp Lys Phe Asp
 35 40 45

Glu His Asp Gly Pro Val Arg Gly Ile Asp Phe His Lys Gln Gln Pro
 50 55 60

Leu Phe Val Ser Gly Gly Asp Asp Tyr Lys Ile Lys Val Trp Asn Tyr
 65 70 75 80

Lys Leu Arg Arg Cys Leu Phe Thr Leu Leu Gly His Leu Asp Tyr Ile
 85 90 95

Arg Thr Thr Phe Phe His His Glu Tyr Pro Trp Ile Leu Ser Ala Ser
 100 105 110

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Asp Asp Gln Thr Ile Arg Val Trp Asn Trp Gln Ser Arg Thr Cys Val
115 120 125

Cys Val Leu Thr Gly His Asn His Tyr Val Met Cys Ala Gln Phe His
130 135 140

Pro Thr Glu Asp Leu Val Val Ser Ala Ser Leu Asp Gln Thr Val Arg
145 150 155 160

Val Trp Asp Ile Ser Gly Leu Arg Lys Lys Asn Leu Ser Pro Gly Ala
165 170 175

Val Glu Ser Asp Val Arg Gly Ile Thr Gly Val Asp Leu Phe Gly Thr
180 185 190

Thr Asp Ala Val Val Lys His Val Leu Glu Gly His Asp Arg Gly Val
195 200 205

Asn Trp Ala Ala Phe His Pro Thr Met Pro Leu Ile Val Ser Gly Ala
210 215 220

Asp Asp Arg Gln Val Lys Ile Trp Arg Met Asn Glu Ser Lys Ala Trp
225 230 235 240

Glu Val Asp Thr Cys Arg Gly His Tyr Asn Asn Val Ser Cys Ala Val
245 250 255

Phe His Pro Arg Gln Glu Leu Ile Leu Ser Asn Ser Glu Asp Lys Ser
260 265 270

Ile Arg Val Trp Asp Met Ser Lys Arg Thr Gly Val Gln Thr Phe Arg
275 280 285

Arg Asp His Asp Arg Phe Trp Val Leu Ala Ala His Pro Asn Leu Asn
290 295 300

Leu Phe Ala Ala Gly His Asp Gly Gly Met Ile Val Phe Lys Leu Glu
305 310 315 320

Arg Glu Arg Pro Ala Tyr Ala Val His Gly Asn Met Leu His Tyr Val
325 330 335

Lys Asp Arg Phe Leu Arg Gln Leu Asp Phe Asn Ser Ser Lys Asp Val
340 345 350

Ala Val Met Gln Leu Arg Ser Gly Ser Lys Phe Pro Val Phe Asn Met
355 360 365

Ser Tyr Asn Pro Ala Glu Asn Ala Val Leu Leu Cys Thr Arg Ala Ser
 370 375 380

Asn Leu Glu Asn Ser Thr Tyr Asp Leu Tyr Thr Ile Pro Lys Asp Ala
 385 390 395 400

Asp Ser Gln Asn Pro Asp Ala Pro Glu Gly Lys Arg Ser Ser Gly Leu
 405 410 415

Thr Ala Val Trp Val Ala Arg Asn Arg Phe Ala Val Leu Asp Arg Met
 420 425 430

His Ser Leu Leu Ile Lys Asn Leu Lys Asn Glu Ile Thr Lys Lys Val
 435 440 445

Gln Val Pro Asn Cys Asp Glu Ile Phe Tyr Ala Gly Thr Gly Asn Leu
 450 455 460

Leu Leu Arg Asp Ala Asp Ser Ile Thr Leu Phe Asp Val Gln Gln Lys
 465 470 475 480

Arg Thr Leu Ala Ser Val Lys Ile Ser Lys Val Lys Tyr Val Ile Trp
 485 490 495

Ser Ala Asp Met Ser His Val Ala Leu Leu Ala Lys His Ala Ile Val
 500 505 510

Ile Cys Asn Arg Lys Leu Asp Ala Leu Cys Asn Ile His Glu Asn Ile
 515 520 525

Arg Val Lys Ser Gly Ala Trp Asp Glu Ser Gly Val Phe Ile Tyr Thr
 530 535 540

Thr Ser Asn His Ile Lys Tyr Ala Val Thr Thr Gly Asp His Gly Ile
 545 550 555 560

Ile Arg Thr Leu Asp Leu Pro Ile Tyr Val Thr Arg Val Lys Gly Asn
 565 570 575

Asn Val Tyr Cys Leu Asp Arg Glu Cys Arg Pro Arg Val Leu Thr Ile
 580 585 590

Asp Pro Thr Glu Phe Lys Phe Lys Leu Ala Leu Ile Asn Arg Lys Tyr
 595 600 605

Asp Glu Val Leu His Met Val Arg Asn Ala Lys Leu Val Gly Gln Ser
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610

Ile Ile Ala Tyr Leu Gln Lys Lys Gly Tyr Pro Glu Val Ala Leu His
625 630 635 640

Phe Val Lys Asp Glu Lys Thr Arg Phe Ser Leu Ala Leu Glu Cys Gly
645 650 655

Asn Ile Glu Ile Ala Leu Glu Ala Ala Lys Ala Leu Asp Asp Lys Asn
660 665 670

Cys Trp Glu Lys Leu Gly Glu Val Ala Leu Leu Gln Gly Asn His Gln
675 680 685

Ile Val Glu Met Cys Tyr Gln Arg Thr Lys Asn Phe Asp Lys Val Ser
690 695 700

Phe Leu Tyr Leu Ile Thr Gly Asn Leu Glu Lys Leu Arg Lys Met Met
705 710 715 720

Lys Ile Ala Glu Ile Arg Lys Asp Met Ser Gly His Tyr Gln Asn Ala
725 730 735

Leu Tyr Leu Gly Asp Val Ser Glu Arg Val Arg Ile Leu Lys Asn Cys
740 745 750

Gly Gln Lys Ser Leu Ala Tyr Leu Thr Ala Ala Thr His Gly Leu Asp
755 760 765

Glu Glu Ala Glu Ser Leu Lys Glu Thr Phe Asp Pro Glu Lys Glu Thr
770 775 780

Ile Pro Asp Ile Asp Pro Asn Ala Lys Leu Leu Gln Pro Pro Ala Pro
785 790 795 800

Ile Met Pro Leu Asp Thr Asn Trp Pro Leu Leu Thr Val Ser Lys Gly
805 810 815

Phe Phe Glu Gly Thr Ile Ala Ser Lys Gly Lys Gly Gly Ala Leu Ala
820 825 830

Ala Asp Ile Asp Ile Asp Thr Val Gly Thr Glu Gly Trp Gly Glu Asp
835 840 845

Ala Glu Leu Gln Leu Asp Glu Asp Gly Phe Val Glu Ala Thr Glu Gly
850 855 860

Leu Gly Asp Asp Ala Leu Gly Lys Gly Gln Glu Glu Gly Gly Trp
 865 870 875 880

Asp Val Glu Glu Asp Leu Glu Leu Pro Pro Glu Leu Asp Ile Ser Pro
 885 890 895

Gly Ala Ala Gly Gly Ala Glu Asp Gly Phe Phe Val Pro Pro Thr Lys
 900 905 910

Gly Thr Ser Pro Thr Gln Ile Trp Cys Asn Asn Ser Gln Leu Pro Val
 915 920 925

Asp His Ile Leu Ala Gly Ser Phe Glu Thr Ala Met Arg Leu Leu His
 930 935 940

Asp Gln Val Gly Val Ile Gln Phe Gly Pro Tyr Lys Gln Leu Phe Leu
 945 950 955 960

Gln Thr Tyr Ala Arg Gly Arg Thr Thr Tyr Gln Ala Leu Pro Cys Leu
 965 970 975

Pro Ser Met Tyr Gly Tyr Pro Asn Arg Asn Trp Lys Asp Ala Gly Leu
 980 985 990

Lys Asn Gly Val Pro Ala Val Gly Leu Lys Leu Asn Asp Leu Ile Gln
 995 1000 1005

Arg Leu Gln Leu Cys Tyr Gln Leu Thr Thr Val Gly Lys Phe Glu
 1010 1015 1020

Glu Ala Val Glu Lys Phe Arg Ser Ile Leu Leu Ser Val Pro Leu
 1025 1030 1035

Leu Val Val Asp Asn Lys Gln Glu Ile Ala Glu Ala Gln Gln Leu
 1040 1045 1050

Ile Thr Ile Cys Arg Glu Tyr Ile Val Gly Leu Ser Val Glu Thr
 1055 1060 1065

Glu Arg Lys Lys Leu Pro Lys Glu Thr Leu Glu Gln Gln Lys Arg
 1070 1075 1080

Ile Cys Glu Met Ala Ala Tyr Phe Thr His Ser Asn Leu Gln Pro
 1085 1090 1095

Val His Met Ile Leu Val Leu Arg Thr Ala Leu Asn Leu Phe Phe
 1100 1105 1110

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Lys Leu Lys Asn Phe Lys Thr Ala Ala Thr Phe Ala Arg Arg Leu
1115 1120 1125

Leu Glu Leu Gly Pro Lys Pro Glu Val Ala Gln Gln Thr Arg Lys
1130 1135 1140

Ile Leu Ser Ala Cys Glu Lys Asn Pro Thr Asp Ala Tyr Gln Leu
1145 1150 1155

Asn Tyr Asp Met His Asn Pro Phe Asp Ile Cys Ala Ala Ser Tyr
1160 1165 1170

Arg Pro Ile Tyr Arg Gly Lys Pro Val Glu Lys Cys Pro Leu Ser
1175 1180 1185

Gly Ala Cys Tyr Ser Pro Glu Phe Lys Gly Gln Ile Cys Arg Val
1190 1195 1200

Thr Thr Val Thr Glu Ile Gly Lys Asp Val Ile Gly Leu Arg Ile
1205 1210 1215

Ser Pro Leu Gln Phe Arg
1220

<210> 17

<211> 1208

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 17

ctggtgagaa gacagcgaaa tggcgctcc ggccccggc ccggcctccg gcggctccgg 60

ggaggtagac gagctgttcg acgtaaagaa cgccttctac atcggcagct accagcagtg 120

cataaacgag gcgcagcggg tgaagctgtc aagcccagag agagacgtgg agagggacgt 180

cttcctgtat agagcgtacc tggcgagag gaagtccggt gtggctcctgg atgagatcaa 240

gccctcctcg gccctgagc tccaggccgt gcgcatgttt gctgactacc tcgcccacga 300

gagtcggagg gacagcatcg tggccgagct ggaccgagag atgagcagga gcgtggacgt 360

gaccaacacc accttcctgc tcatggccgc ctccatctat ctccacgacc agaaccggga 420

tgccgccctg cgtgcgctgc accaggggga cagcctggag tgcacagcca tgacagtgca 480

gatcctgctg aagctggacc gcctggacct cgcccgaag gagctgaaga gaatgcagga 540

cctggacgag gatgccaccc tcaccagct cgccactgcc tgggtcagcc tggccacggg 600

tggtgagaag ctgcaggatg cctactacat cttccaggag atggctgaca agtgctcgcc 660

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caacctcatc gtcctgtccc agcacctggg caagccccct gaggtgacaa accgatacct      840
gtcccagctg aaggatgccc acagggtccc tcccttcac aaggagtacc aggccaagga      900
gaacgacttt gacaggctgg tgctacagta cgctcccagc gcctgaggct ggcccagagc      960
tgtcaggacc atgaagccag gacagaggcc aggagccagc cctgcagccc tccccacccg     1020
gcatccacct gcatcccctc tgggggcagg agcccacccc cagcaccccc atctgttaat     1080
aaatatctca actccagggt gttccacctg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     1140
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa     1200
aaaaaaaaaa                                     1208

```

<210> 18

<211> 308

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 18

```

Met Ala Pro Pro Ala Pro Gly Pro Ala Ser Gly Gly Ser Gly Glu Val
1          5          10          15

```

```

Asp Glu Leu Phe Asp Val Lys Asn Ala Phe Tyr Ile Gly Ser Tyr Gln
          20          25          30

```

```

Gln Cys Ile Asn Glu Ala Gln Arg Val Lys Leu Ser Ser Pro Glu Arg
          35          40          45

```

```

Asp Val Glu Arg Asp Val Phe Leu Tyr Arg Ala Tyr Leu Ala Gln Arg
          50          55          60

```

```

Lys Phe Gly Val Val Leu Asp Glu Ile Lys Pro Ser Ser Ala Pro Glu
65          70          75          80

```

```

Leu Gln Ala Val Arg Met Phe Ala Asp Tyr Leu Ala His Glu Ser Arg
          85          90          95

```

```

Arg Asp Ser Ile Val Ala Glu Leu Asp Arg Glu Met Ser Arg Ser Val
          100          105          110

```

```

Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala Ala Ser Ile Tyr Leu
          115          120          125

```


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His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala Leu His Gln Gly Asp
130 135 140

Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile Leu Leu Lys Leu Asp
145 150 155 160

Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg Met Gln Asp Leu Asp
165 170 175

Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala Trp Val Ser Leu Ala
180 185 190

Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr Ile Phe Gln Glu Met
195 200 205

Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu Asn Gly Gln Ala Ala
210 215 220

Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala Glu Gly Leu Leu Gln
225 230 235 240

Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu Thr Leu Val Asn Leu
245 250 255

Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro Glu Val Thr Asn Arg
260 265 270

Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser His Pro Phe Ile Lys
275 280 285

Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg Leu Val Leu Gln Tyr
290 295 300

Ala Pro Ser Ala
305

<210> 19

<211> 3528

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 19

agccaaggac tctggagccg ccgccgccgc tgctgcggtt catatccgga gtagacggag 60

ccgcagtaga cggatccgcg gctgcaccaa accactgccc ctcggagcct ggtagtgggc 120

cacaagcccc cagtcccaga ggcgtggtgg gtcgggcaga gtcggaagaa ctggctttct 180

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| | |
|---|------|
| agctggaaga tgcggaaggg gagcgactag gccgcttgcg tctgggcctg gcagaagggg | 240 |
| ccggatttttc tggcatcctt aaatcttggtg tcaaggattg gttataatat aaccagaaac | 300 |
| catgacggcg gctgagaacg tatgctacac gttaattaac gtgccaatgg attcagaacc | 360 |
| accatctgaa attagcttaa aaaatgatct agaaaaagga gatgtaaagt caaagactga | 420 |
| agctttgaag aaagtaatca ttatgattct gaatggtgaa aaacttcctg gacttctgat | 480 |
| gaccatcatt cgttttgtgc tacctcttca ggatcacact atcaagaaat tacttctggt | 540 |
| atthtgggaa attgttccta aaacaactcc agatgggaga cttttacatg agatgatcct | 600 |
| tgtatgtgat gcatacagaa aggatcttca acatcctaata gaatttattc gaggatctac | 660 |
| tcttcgtttt ctttgcaaata tgaaagaagc agaattgcta gaacctttaa tgccagctat | 720 |
| tcgtgcatgt ttggagcatc gacacagcta tgttagaaga aatgctgttt tggccatcta | 780 |
| taccatctat agaaattttg aacatcttat acctgatgct cctgaactga tacatgattt | 840 |
| tctggtgaat gagaaggatg caagttgcaa aaggaatgca tttatgatgc taattcatgc | 900 |
| agatcaggat cgagcttttg attacttaag tacttgcatt gatcaagttc aaacatttgg | 960 |
| agacattctg cagctgggta ttgttgaaact gatttataag gtctgtcatg ctaatccatc | 1020 |
| agaaagagct cgtttttattc gctgcatcta taacttatta cagtcacca gccctgctgt | 1080 |
| aaaatatgaa gctgctggga cattagtac actctctagt gcaccaactg caatcaaggc | 1140 |
| tgctgctcag tgttacattg atttaattat taaggagagc gacaacaatg taaaactcat | 1200 |
| agttttggat cgcttgatag aattaaaaga gcatcctgct catgaacgag tactacagga | 1260 |
| tctggttatg gatataccta gagtattgag cacaccagac ttagaagtac gaaagaaaac | 1320 |
| tctgcagtta gactggatc ttgtctcttc tagaaatgtt gaagagctgg ttattgtcct | 1380 |
| gaagaaggaa gtgataaaaa caaataatgt gtctgagcat gaagatactg acaaatacag | 1440 |
| acaactccta gtgcgaacat tgcattcctg ttctgtccga tttccagata tggctgcaaa | 1500 |
| tgttattcct gtgttaatgg aatttctcag tgacaacaac gaagcagcag ctgctgatgt | 1560 |
| cttggagttt gttcgtgaag ccattcagcg ctttgataac ctgagaatgc ttattgttga | 1620 |
| gaagatgctt gaagtctttc atgctattaa atctgtcaag atttaccgag gagcattatg | 1680 |
| gatcctggga gaatactgta gtaccaagga agacattcag agtgtgatga ctgagatccg | 1740 |
| cagggtccctt ggagagatcc caattgtaga gtcagaaata aagaaagaag ctggtgaatt | 1800 |
| aaaacctgaa gaagaaataa ctgtagggcc agttcagaaa ttggttactg aaatgggtac | 1860 |
| ctatgcaact cagagtgcct ttagcagttc tagaccacc aagaaagagg aagacagacc | 1920 |
| tcccttgaga ggattccttc tggatggaga tttctttgtt gctgcctccc ttgccacaac | 1980 |
| tctgaccaag attgcattgc gctatgtagc tttggttcag gagaagaaaa agcaaaattc | 2040 |

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| | |
|--|------|
| ttttgttgct gaggctatgt tgctcatggc tactatcctg catttgggaa aatcctctct | 2100 |
| tcctaagaag ccaattactg atgatgatgt ggatcgaatt tccctgtgcc tcaaggtctt | 2160 |
| gtctgaatgt tcacctttaa tgaatgacat tttcaataag gaatgcagac agtccctttc | 2220 |
| tcacatgtta tctgctaaac tagaagaaga gaaattatcc caaaagaaag aatctgaaaa | 2280 |
| gaggaatgtg acagtacagc ctgatgacct catttccttc atgcaactaa ctgctaagaa | 2340 |
| tgaaatgaac tgcaaggaag atcagtttca gctgagttaa ctggcagcaa tgggtaacac | 2400 |
| acagaggaaa gaggcagcag atcccctagc atctaaactt aacaaggcca cccaattgac | 2460 |
| aggttttctca gatcctgtat atgcagaagc ttacgttcat gtcaaccaat atgatattgt | 2520 |
| cctggatgta cttgttgatga accaaaccag tgatactttg cagaattgca cattagaact | 2580 |
| agctacacta ggggatctga aacttggtga aaagccgtct ctttgactc ttgctcctca | 2640 |
| tgacttcgca aatattaaag ctaacgtcaa agtagcatca acagaaaatg gaataatttt | 2700 |
| tggtaatata gtttatgatg tctctggagc agcaagtgc agaaattgtg tggttctcag | 2760 |
| tgatattcac atcgacatca tggactatat ccagcctgca acttgactg atgcagaatt | 2820 |
| ccgtcagatg tgggccgaat ttgaatggga aaacaaagt acagttaaca ccaacatggg | 2880 |
| tgatttaaat gactacttac agcacatatt aaagtcaacc aatatgaaat gcctgactcc | 2940 |
| agaaaaggcc ctttctgggt actgtggctt tatggcagcc aacctttatg ctcgttccat | 3000 |
| atgttggtgaa gatgcacttg caaatgtcag cattgagaag ccaattcacc aggaccaga | 3060 |
| tgctgctgtt accggccata taagaattcg tgcaagagc cagggaatgg ccttaagtct | 3120 |
| tggagataaa atcaacttgt cacagaagaa aactagtata taaaaataaa caaaaagtcc | 3180 |
| ttgaagcttt acagttaatt taggtatggg cttactggac tccaacatct tttgtactct | 3240 |
| ttcatgctta tatagaatct gagttcatgc tgaatacttt tcagccaata atttatagcc | 3300 |
| tttcccttaa atcaagattg agtttaaaat tatagtttgt cttttgtctt aacagttctg | 3360 |
| aatgctgtcc tcaaagtata taatgtttca tgtaccaaga cccttttcac agtacaataa | 3420 |
| acagatctat tcataaattt ttgttatatt ataaataaat gattacataa ttttagttat | 3480 |
| aaaaaaaaa aaaaaaaaaa agaaaaaaaa aaaaaaaaaa aaaaaaaa | 3528 |

<210> 20

<211> 953

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 20

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Ala | Ala | Glu | Asn | Val | Cys | Tyr | Thr | Leu | Ile | Asn | Val | Pro | Met |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Asp Ser Glu Pro Pro Ser Glu Ile Ser Leu Lys Asn Asp Leu Glu Lys
20 25 30

Gly Asp Val Lys Ser Lys Thr Glu Ala Leu Lys Lys Val Ile Ile Met
35 40 45

Ile Leu Asn Gly Glu Lys Leu Pro Gly Leu Leu Met Thr Ile Ile Arg
50 55 60

Phe Val Leu Pro Leu Gln Asp His Thr Ile Lys Lys Leu Leu Leu Val
65 70 75 80

Phe Trp Glu Ile Val Pro Lys Thr Thr Pro Asp Gly Arg Leu Leu His
85 90 95

Glu Met Ile Leu Val Cys Asp Ala Tyr Arg Lys Asp Leu Gln His Pro
100 105 110

Asn Glu Phe Ile Arg Gly Ser Thr Leu Arg Phe Leu Cys Lys Leu Lys
115 120 125

Glu Ala Glu Leu Leu Glu Pro Leu Met Pro Ala Ile Arg Ala Cys Leu
130 135 140

Glu His Arg His Ser Tyr Val Arg Arg Asn Ala Val Leu Ala Ile Tyr
145 150 155 160

Thr Ile Tyr Arg Asn Phe Glu His Leu Ile Pro Asp Ala Pro Glu Leu
165 170 175

Ile His Asp Phe Leu Val Asn Glu Lys Asp Ala Ser Cys Lys Arg Asn
180 185 190

Ala Phe Met Met Leu Ile His Ala Asp Gln Asp Arg Ala Leu Asp Tyr
195 200 205

Leu Ser Thr Cys Ile Asp Gln Val Gln Thr Phe Gly Asp Ile Leu Gln
210 215 220

Leu Val Ile Val Glu Leu Ile Tyr Lys Val Cys His Ala Asn Pro Ser
225 230 235 240

Glu Arg Ala Arg Phe Ile Arg Cys Ile Tyr Asn Leu Leu Gln Ser Ser
245 250 255

Ser Pro Ala Val Lys Tyr Glu Ala Ala Gly Thr Leu Val Thr Leu Ser

Ser Ala Pro Thr Ala Ile Lys Ala Ala Ala Gln Cys Tyr Ile Asp Leu
275 280 285

Ile Ile Lys Glu Ser Asp Asn Asn Val Lys Leu Ile Val Leu Asp Arg
290 295 300

Leu Ile Glu Leu Lys Glu His Pro Ala His Glu Arg Val Leu Gln Asp
305 310 315 320

Leu Val Met Asp Ile Leu Arg Val Leu Ser Thr Pro Asp Leu Glu Val
325 330 335

Arg Lys Lys Thr Leu Gln Leu Ala Leu Asp Leu Val Ser Ser Arg Asn
340 345 350

Val Glu Glu Leu Val Ile Val Leu Lys Lys Glu Val Ile Lys Thr Asn
355 360 365

Asn Val Ser Glu His Glu Asp Thr Asp Lys Tyr Arg Gln Leu Leu Val
370 375 380

Arg Thr Leu His Ser Cys Ser Val Arg Phe Pro Asp Met Ala Ala Asn
385 390 395 400

Val Ile Pro Val Leu Met Glu Phe Leu Ser Asp Asn Asn Glu Ala Ala
405 410 415

Ala Ala Asp Val Leu Glu Phe Val Arg Glu Ala Ile Gln Arg Phe Asp
420 425 430

Asn Leu Arg Met Leu Ile Val Glu Lys Met Leu Glu Val Phe His Ala
435 440 445

Ile Lys Ser Val Lys Ile Tyr Arg Gly Ala Leu Trp Ile Leu Gly Glu
450 455 460

Tyr Cys Ser Thr Lys Glu Asp Ile Gln Ser Val Met Thr Glu Ile Arg
465 470 475 480

Arg Ser Leu Gly Glu Ile Pro Ile Val Glu Ser Glu Ile Lys Lys Glu
485 490 495

Ala Gly Glu Leu Lys Pro Glu Glu Glu Ile Thr Val Gly Pro Val Gln
500 505 510

Lys Leu Val Thr Glu Met Gly Thr Tyr Ala Thr Gln Ser Ala Leu Ser
515 520 525

Ser Ser Arg Pro Thr Lys Lys Glu Glu Asp Arg Pro Pro Leu Arg Gly
530 535 540

Phe Leu Leu Asp Gly Asp Phe Phe Val Ala Ala Ser Leu Ala Thr Thr
545 550 555 560

Leu Thr Lys Ile Ala Leu Arg Tyr Val Ala Leu Val Gln Glu Lys Lys
565 570 575

Lys Gln Asn Ser Phe Val Ala Glu Ala Met Leu Leu Met Ala Thr Ile
580 585 590

Leu His Leu Gly Lys Ser Ser Leu Pro Lys Lys Pro Ile Thr Asp Asp
595 600 605

Asp Val Asp Arg Ile Ser Leu Cys Leu Lys Val Leu Ser Glu Cys Ser
610 615 620

Pro Leu Met Asn Asp Ile Phe Asn Lys Glu Cys Arg Gln Ser Leu Ser
625 630 635 640

His Met Leu Ser Ala Lys Leu Glu Glu Glu Lys Leu Ser Gln Lys Lys
645 650 655

Glu Ser Glu Lys Arg Asn Val Thr Val Gln Pro Asp Asp Pro Ile Ser
660 665 670

Phe Met Gln Leu Thr Ala Lys Asn Glu Met Asn Cys Lys Glu Asp Gln
675 680 685

Phe Gln Leu Ser Leu Leu Ala Ala Met Gly Asn Thr Gln Arg Lys Glu
690 695 700

Ala Ala Asp Pro Leu Ala Ser Lys Leu Asn Lys Val Thr Gln Leu Thr
705 710 715 720

Gly Phe Ser Asp Pro Val Tyr Ala Glu Ala Tyr Val His Val Asn Gln
725 730 735

Tyr Asp Ile Val Leu Asp Val Leu Val Val Asn Gln Thr Ser Asp Thr
740 745 750

Leu Gln Asn Cys Thr Leu Glu Leu Ala Thr Leu Gly Asp Leu Lys Leu
755 760 765

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Val Glu Lys Pro Ser Pro Leu Thr Leu Ala Pro His Asp Phe Ala Asn
770 775 780

Ile Lys Ala Asn Val Lys Val Ala Ser Thr Glu Asn Gly Ile Ile Phe
785 790 795 800

Gly Asn Ile Val Tyr Asp Val Ser Gly Ala Ala Ser Asp Arg Asn Cys
805 810 815

Val Val Leu Ser Asp Ile His Ile Asp Ile Met Asp Tyr Ile Gln Pro
820 825 830

Ala Thr Cys Thr Asp Ala Glu Phe Arg Gln Met Trp Ala Glu Phe Glu
835 840 845

Trp Glu Asn Lys Val Thr Val Asn Thr Asn Met Val Asp Leu Asn Asp
850 855 860

Tyr Leu Gln His Ile Leu Lys Ser Thr Asn Met Lys Cys Leu Thr Pro
865 870 875 880

Glu Lys Ala Leu Ser Gly Tyr Cys Gly Phe Met Ala Ala Asn Leu Tyr
885 890 895

Ala Arg Ser Ile Phe Gly Glu Asp Ala Leu Ala Asn Val Ser Ile Glu
900 905 910

Lys Pro Ile His Gln Gly Pro Asp Ala Ala Val Thr Gly His Ile Arg
915 920 925

Ile Arg Ala Lys Ser Gln Gly Met Ala Leu Ser Leu Gly Asp Lys Ile
930 935 940

Asn Leu Ser Gln Lys Lys Thr Ser Ile
945 950

<210> 21
<211> 3075
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 21
ggcactgtag caccgtact ccgtgccgcg cccgtcgagc attgcgttgc tgcattgcgc 60
cccaccgact ccactatggt gaagaaattc gacaagaagg atgaggagtc aggtggaggc 120
tccaacccat tccagcacct tgagaagagt gcggtactcc aggaggcccg tgtatttaat 180

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| | |
|--|------|
| gaaactccca tcaaccctcg gaaatgtgcc cacatcctca ccaagattct ttatctcata | 240 |
| aaccaggggg agcacctggg gaccacggaa gcgaccgagg ctttctttgc catgaccaag | 300 |
| ctctttcagt ccaatgaccc cacactccgt cggatgtgct acttgacat caaggagatg | 360 |
| tcttgattg cagaggatgt catcattgtc accagcagcc taacaaaaga catgactggg | 420 |
| aaagaagaca actaccgggg cccggccgtg cgagccctct gccagatcac tgatagcacc | 480 |
| atgctgcagg ctattgagcg ctacatgaaa caagccattg tggacaaggt gcccagtgtc | 540 |
| tccagctctg ccctcgtgtc ttccttgac ctgctgaagt gcagctttga cgtggccaag | 600 |
| cgctgggtga atgaggctca ggaggcagca tccagtata acatcatggt ccagtaccac | 660 |
| gcactagggc tcctgtacca tgtgcgtaag aatgaccgcc tagccgtcaa taagatgatc | 720 |
| agcaaggcca cacggcatgg ccttaagtct ccctttgcct actgcatgat gatccgggtg | 780 |
| gccagcaagc agctggaaga ggaggatggc agccgtgaca gccactggt tgacttcac | 840 |
| gagagctgct tgcgcaacaa gcacgagatg gtggtgtatg aagccgcctc ggccattgtc | 900 |
| aacctgcctg ggtgcagcgc caaggagctg gccccagctg tctcagtgtc ccagctcttc | 960 |
| tgcagctccc ccaaggccgc cctccgttac gccgccgtcc gcaccctcaa caaggaggcc | 1020 |
| atgaagcacc cgtccgctgt gacagcttgt aatctggatc tggagaacct ggtcacagat | 1080 |
| tcaaaccgca gcattgccac gctggccatc accaccctcc ttaagacggg cagcgagagc | 1140 |
| agcatcgacc gcctcatgaa gcagatctcc tccttcattg cagaaatctc ggatgaattc | 1200 |
| aagggtggtg ttgtccaggc catcagtgcc ctgtgtcaga aatatcctcg caaacacgcc | 1260 |
| gtccttatga acttcctgtt caccatgctg cgggaagagg gtggctttga gtataagcgc | 1320 |
| gctatcgtgg actgcatcat cagcatcatt gaagagaact cagagagcaa ggagacaggg | 1380 |
| ctgtcacatc tgtgcgagtt catcgaggac tgcgagttca cagtgtggc caccctgatt | 1440 |
| ctacatctcc tgggccagga ggggcccag accaccaatc cctcaaagta catccgcttc | 1500 |
| atctataacc gagtgggtctt ggagcatgag gaggtccggg cagggtgctgt gagggtctctg | 1560 |
| gcgaagtttg gagcccagaa tgaagagatg ttaccagta tcttggtgtt gctgaagagg | 1620 |
| tgtgtgatgg atgatgacaa tgaagtaagg gaccgagcca cttctacct aaatgtcctg | 1680 |
| gagcagaagc agaaggccct taatgcaggc tatatcctaa atggtctgac tgtgtccatc | 1740 |
| cctgggtctgg agagggtctt gcagcagtag actctagaac catcagaaaa accttttgac | 1800 |
| ctcaagtctg tgcccctggc cacggcgccc atggcagagc agagaacaga aagtaccccc | 1860 |
| atcacagcag tcaaacagcc tgagaaagtg gcagctacca ggcaggagat cttccaggag | 1920 |
| cagttggcag cagtgccaga gttccgcggt cttgggcccc tcttcaagtc ctcgcctgag | 1980 |
| cccgtggccc tcaccgagtc agagacggag tatgtcatcc gctgcaccaa acacaccttc | 2040 |

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| | |
|---|------|
| accaaaccaca tggttttttca gtttgactgc acaaacacac tcaatgacca gaccttggag | 2100 |
| aatgtcacag tgcagatgga gcccactgag gcctatgagg tgctctgtta cgtgcctgcc | 2160 |
| cggagcctgc cctacaacca gcccgggacc tgctacacac tggtggcact gcccaaagaa | 2220 |
| gacccacag ctgtggcctg cacattcagc tgcattgatga agttcactgt caaggactgt | 2280 |
| gatccaccca ctggggagac tgatgacgaa ggctatgagg atgagtatgt gctggaagat | 2340 |
| ctggaagtta ctgtagctga tcacattcaa aaggtcatga aactgaactt cgaagcagcc | 2400 |
| tgggatgagg taggggatga atttgagaag gaggaacgt tcacctgtc taccatcaag | 2460 |
| acacttgaag aggctgtggg taatattgtg aagttcttgg gaatgcaccc ttgtgagagg | 2520 |
| tcagacaaag tgccggataa caagaacacc cacacgttgc tcctggctgg tgtgttcgg | 2580 |
| ggtggtcatg acatcctggt gcgctcccg ctgctgcttt tggacacagt gacaatgcag | 2640 |
| gtgacagcca gaagtttga ggagctgcca gtagacatca tcttggcatc tgtgggataa | 2700 |
| gagggcagcc tgcattggac ctcataccct tccccaacac tacctggaag ttgtgccttc | 2760 |
| ctcatgaaac tggcagaaac cccttcccaa gcttctgtat tgaaaaacaa ttaggaatca | 2820 |
| ttgcagattt tttttattc tgctcccacc tcccaccgg gactacttgc tggtgacttt | 2880 |
| tttttttttt ttttttaaat aggggatgat tttagcttgt cctaaatctt gctgtccacc | 2940 |
| cttccaggaa agggacattg taaatgaata aaacattctc aactcctctt gaatctatcc | 3000 |
| ccaagaaac catcttatcc ctgtaataaa tcagcatgta ttattgaaa aaaaaaaaaa | 3060 |
| aaaaaaaaa aaaaa | 3075 |

<210> 22
 <211> 874
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 22

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Leu | Lys | Lys | Phe | Asp | Lys | Lys | Asp | Glu | Glu | Ser | Gly | Gly | Gly | Ser |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Pro | Phe | Gln | His | Leu | Glu | Lys | Ser | Ala | Val | Leu | Gln | Glu | Ala | Arg |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Asn | Glu | Thr | Pro | Ile | Asn | Pro | Arg | Lys | Cys | Ala | His | Ile | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Lys | Ile | Leu | Tyr | Leu | Ile | Asn | Gln | Gly | Glu | His | Leu | Gly | Thr | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |

Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Lys Leu Phe Gln Ser Asn
65 70 75 80

Asp Pro Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ser
85 90 95

Cys Ile Ala Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp
100 105 110

Met Thr Gly Lys Glu Asp Asn Tyr Arg Gly Pro Ala Val Arg Ala Leu
115 120 125

Cys Gln Ile Thr Asp Ser Thr Met Leu Gln Ala Ile Glu Arg Tyr Met
130 135 140

Lys Gln Ala Ile Val Asp Lys Val Pro Ser Val Ser Ser Ser Ala Leu
145 150 155 160

Val Ser Ser Leu His Leu Leu Lys Cys Ser Phe Asp Val Val Lys Arg
165 170 175

Trp Val Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val
180 185 190

Gln Tyr His Ala Leu Gly Leu Leu Tyr His Val Arg Lys Asn Asp Arg
195 200 205

Leu Ala Val Asn Lys Met Ile Ser Lys Val Thr Arg His Gly Leu Lys
210 215 220

Ser Pro Phe Ala Tyr Cys Met Met Ile Arg Val Ala Ser Lys Gln Leu
225 230 235 240

Glu Glu Glu Asp Gly Ser Arg Asp Ser Pro Leu Phe Asp Phe Ile Glu
245 250 255

Ser Cys Leu Arg Asn Lys His Glu Met Val Val Tyr Glu Ala Ala Ser
260 265 270

Ala Ile Val Asn Leu Pro Gly Cys Ser Ala Lys Glu Leu Ala Pro Ala
275 280 285

Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Ala Ala Leu Arg
290 295 300

Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser
305 310 315 320

Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Val Thr Asp Ser
325 330 335

Asn Arg Ser Ile Ala Thr Leu Ala Ile Thr Thr Leu Leu Lys Thr Gly
340 345 350

Ser Glu Ser Ser Ile Asp Arg Leu Met Lys Gln Ile Ser Ser Phe Met
355 360 365

Ser Glu Ile Ser Asp Glu Phe Lys Val Val Val Val Gln Ala Ile Ser
370 375 380

Ala Leu Cys Gln Lys Tyr Pro Arg Lys His Ala Val Leu Met Asn Phe
385 390 395 400

Leu Phe Thr Met Leu Arg Glu Glu Gly Gly Phe Glu Tyr Lys Arg Ala
405 410 415

Ile Val Asp Cys Ile Ile Ser Ile Ile Glu Glu Asn Ser Glu Ser Lys ...
420 425 430

Glu Thr Gly Leu Ser His Leu Cys Glu Phe Ile Glu Asp Cys Glu Phe
435 440 445

Thr Val Leu Ala Thr Arg Ile Leu His Leu Leu Gly Gln Glu Gly Pro
450 455 460

Lys Thr Thr Asn Pro Ser Lys Tyr Ile Arg Phe Ile Tyr Asn Arg Val
465 470 475 480

Val Leu Glu His Glu Glu Val Arg Ala Gly Ala Val Ser Ala Leu Ala
485 490 495

Lys Phe Gly Ala Gln Asn Glu Glu Met Leu Pro Ser Ile Leu Val Leu
500 505 510

Leu Lys Arg Cys Val Met Asp Asp Asp Asn Glu Val Arg Asp Arg Ala
515 520 525

Thr Phe Tyr Leu Asn Val Leu Glu Gln Lys Gln Lys Ala Leu Asn Ala
530 535 540

Gly Tyr Ile Leu Asn Gly Leu Thr Val Ser Ile Pro Gly Leu Glu Arg
545 550 555 560

Ala Leu Gln Gln Tyr Thr Leu Glu Pro Ser Glu Lys Pro Phe Asp Leu
565 570 575

Lys Ser Val Pro Leu Ala Thr Ala Pro Met Ala Glu Gln Arg Thr Glu
580 585 590

Ser Thr Pro Ile Thr Ala Val Lys Gln Pro Glu Lys Val Ala Ala Thr
595 600 605

Arg Gln Glu Ile Phe Gln Glu Gln Leu Ala Ala Val Pro Glu Phe Arg
610 615 620

Gly Leu Gly Pro Leu Phe Lys Ser Ser Pro Glu Pro Val Ala Leu Thr
625 630 635 640

Glu Ser Glu Thr Glu Tyr Val Ile Arg Cys Thr Lys His Thr Phe Thr
645 650 655

Asn His Met Val Phe Gln Phe Asp Cys Thr Asn Thr Leu Asn Asp Gln
660 665 670

Thr Leu Glu Asn Val Thr Val Gln Met Glu Pro Thr Glu Ala Tyr Glu
675 680 685

Val Leu Cys Tyr Val Pro Ala Arg Ser Leu Pro Tyr Asn Gln Pro Gly
690 695 700

Thr Cys Tyr Thr Leu Val Ala Leu Pro Lys Glu Asp Pro Thr Ala Val
705 710 715 720

Ala Cys Thr Phe Ser Cys Met Met Lys Phe Thr Val Lys Asp Cys Asp
725 730 735

Pro Thr Thr Gly Glu Thr Asp Asp Glu Gly Tyr Glu Asp Glu Tyr Val
740 745 750

Leu Glu Asp Leu Glu Val Thr Val Ala Asp His Ile Gln Lys Val Met
755 760 765

Lys Leu Asn Phe Glu Ala Ala Trp Asp Glu Val Gly Asp Glu Phe Glu
770 775 780

Lys Glu Glu Thr Phe Thr Leu Ser Thr Ile Lys Thr Leu Glu Glu Ala
785 790 795 800

Val Gly Asn Ile Val Lys Phe Leu Gly Met His Pro Cys Glu Arg Ser
805 810 815

Asp Lys Val Pro Asp Asn Lys Asn Thr His Thr Leu Leu Leu Ala Gly
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Val Phe Arg Gly Gly His Asp Ile Leu Val Arg Ser Arg Leu Leu Leu
835 840 845

Leu Asp Thr Val Thr Met Gln Val Thr Ala Arg Ser Leu Glu Glu Leu
850 855 860

Pro Val Asp Ile Ile Leu Ala Ser Val Gly
865 870

<210> 23
<211> 3110
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

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catctggaga agagtgcgtg ttacaggag gctcgtatat tcaatgaaac tccaatcaat 180
ccaagaagat gtttgcata tcttacaag attctttact tactgaacca gggatgaacac 240
tttgaacaa cggaagctac agaagcctt tttgcaatga cgcgattgtt tcaatctaata 300
gatcaaacat tgaggagaat gtgctacctt accatcaaag aaatggctac catctctgag 360
gatgtgataa ttgtcacaag cagtctgact aaagacatga ctggaaaaga agatgtatac 420
cgaggcccg ccatcagagc tctctgcagg atcaccgatg gaacaatgtt gcaagccatt 480
gaaagataca tgaagcaggc cattgtggat aaagtttcca gtgtatccag ttcagcactg 540
gtatcttccc tgcacatgat gaagataagc tatgatgtgg ttaagcgctg gatcaatgaa 600
gccaagaag ctgcatcaag tgataatatt atggtccagt accatgcatt gggagtcctg 660
tatcacctta gaaagaatga tgcacttgct gtttccaaga tgttgaataa gtttactaaa 720
tctggtctca agtcacagtt tgcttactgc atgctgatcc gaattgccag tcgcttacta 780
aaagaaactg aggatggcca tgaaagtcca ctgtttgatt tcattgagag ctgcttgcca 840
aataaacatg aaatgggtat ttatgaagct gcttcagcta tcatccatct tcctaactgc 900
actgcaagag agttggcacc tgctgtttca gttcttcaac ttttctgtag ttctcctaag 960
ccagccttga gatatgcagc tgtgaggacc ttgaacaagg tggcaatgaa gcacccctct 1020
gctgttactg cctgcaatct ggacttagaa aacttaatca cagactcaa cagaagcatt 1080
gctaccttag ccattactac actcctcaa acaggaagtg agagcagtggt ggaccggctc 1140
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| | | | | | | |
|------------|------------|-------------|-------------|-------------|-------------|------|
| caggcaatta | gtgctctctg | tcagaaatac | cctcgaaagc | acagtgtcat | gatgactttc | 1260 |
| ctctccaaca | tgctccgaga | tgatggaggc | tttgagtaca | agcgggcat | tgtggactgt | 1320 |
| ataatcagca | ttgtggaaga | gaaccctgag | agtaaagaag | caggcctagc | ccacctttgt | 1380 |
| gaattcattg | aggactgtga | acacactggt | ctggctacta | agattctaca | cttgttgggc | 1440 |
| aaagagggcc | ctagaacgcc | tgtccctcc | aaatatatcc | gttttatttt | taataggggt | 1500 |
| gtcctggaga | atgaggctgt | cagagctgct | gctgtgagt | ctttggctaa | atttggggct | 1560 |
| cagaatgaga | gtcttctccc | aagcatcctt | gtactcttac | agagggtgat | gatggatact | 1620 |
| gatgacgagg | tacgagacag | agctaccttc | tatctgaatg | tgctgcagca | gaggcagatg | 1680 |
| gcactaaatg | ccacatatat | ctttaatggt | ttgacggctt | ctgtaccagg | gatggaaaaa | 1740 |
| gccttacacc | agtacacgtt | ggagccttca | gaaaaaccgt | ttgacatgaa | atcaattcct | 1800 |
| cttgctatgg | ctcctgtctt | tgaacagaaa | gcagaaatca | cacttggtggc | tactaagcca | 1860 |
| gagaagttgg | ctccttccag | gcaagacatt | ttccaagaac | aattggctgc | cattcctgag | 1920 |
| tttctgaata | taggaccctt | gttcaagtct | tctgagcctg | ttcaacttac | agaagcagag | 1980 |
| acagaatatt | ttgttcgatg | tatcaagcac | atgtttacca | atcacatcgt | gttccagttt | 2040 |
| gactgcacca | acactctcaa | tgaccagctg | ctggaaaaag | tgacagtgca | gatggagcca | 2100 |
| tcagattcct | atgaagtgtt | gtcttgtatc | ccagcccca | gccttcctta | taaccaacca | 2160 |
| ggaatatgtt | acactcttgt | tcgtttgcct | gatgatgacc | ctacagcagt | tgcaggctcc | 2220 |
| tttagctgca | ccatgaagtt | tacagtccgg | gactgtgacc | ctaacttg | agttccagat | 2280 |
| gaggatgggt | atgatgatga | gtatgtgctg | gaagatctcg | aagtgactgt | gtctgaccat | 2340 |
| attcagaaag | tactgaagcc | taactttgct | gctgcttggg | aagagggtggg | agataccttt | 2400 |
| gagaaagagg | aaacctttgc | cctcagttct | acaaaaccc | ttgaagaggc | tgtcaacaat | 2460 |
| atcatcacat | ttctgggcat | gcagccatgt | gagagggtccg | ataaagtacc | tgagaacaag | 2520 |
| aattcccatt | cgctctatct | ggcagggtata | ttcagagggtg | gctatgattt | attgggtgagg | 2580 |
| tccaggctgg | ccttagccga | tggagtgacc | atgcagggtga | ctgtcagaag | taaagagaga | 2640 |
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| actccagctg | cttaacttca | ttttattctt | taatgtgtac | ctgaaagctc | ctggcaatgc | 3000 |
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ttgtcacaaat tcatttttat taatagaaaa taaacactta ttccagtttc

3110

<210> 24

<211> 871

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 24

Met Ile Lys Lys Phe Asp Lys Lys Asp Glu Glu Ser Gly Ser Gly Ser
 1 5 10 15

Asn Pro Phe Gln His Leu Glu Lys Ser Ala Val Leu Gln Glu Ala Arg
 20 25 30

Ile Phe Asn Glu Thr Pro Ile Asn Pro Arg Arg Cys Leu His Ile Leu
 35 40 45

Thr Lys Ile Leu Tyr Leu Leu Asn Gln Gly Glu His Phe Gly Thr Thr
 50 55 60

Glu Ala Thr Glu Ala Phe Phe Ala Met Thr Arg Leu Phe Gln Ser Asn
 65 70 75 80

Asp Gln Thr Leu Arg Arg Met Cys Tyr Leu Thr Ile Lys Glu Met Ala
 85 90 95

Thr Ile Ser Glu Asp Val Ile Ile Val Thr Ser Ser Leu Thr Lys Asp
 100 105 110

Met Thr Gly Lys Glu Asp Val Tyr Arg Gly Pro Ala Ile Arg Ala Leu
 115 120 125

Cys Arg Ile Thr Asp Gly Thr Met Leu Gln Ala Ile Glu Arg Tyr Met
 130 135 140

Lys Gln Ala Ile Val Asp Lys Val Ser Ser Val Ser Ser Ser Ala Leu
 145 150 155 160

Val Ser Ser Leu His Met Met Lys Ile Ser Tyr Asp Val Val Lys Arg
 165 170 175

Trp Ile Asn Glu Ala Gln Glu Ala Ala Ser Ser Asp Asn Ile Met Val
 180 185 190

Gln Tyr His Ala Leu Gly Val Leu Tyr His Leu Arg Lys Asn Asp Arg
 195 200 205

Leu Ala Val Ser Lys Met Leu Asn Lys Phe Thr Lys Ser Gly Leu Lys
 210 215 220

Ser Gln Phe Ala Tyr Cys Met Leu Ile Arg Ile Ala Ser Arg Leu Leu
 225 230 235 240

Lys Glu Thr Glu Asp Gly His Glu Ser Pro Leu Phe Asp Phe Ile Glu
 245 250 255

Ser Cys Leu Arg Asn Lys His Glu Met Val Ile Tyr Glu Ala Ala Ser
 260 265 270

Ala Ile Ile His Leu Pro Asn Cys Thr Ala Arg Glu Leu Ala Pro Ala
 275 280 285

Val Ser Val Leu Gln Leu Phe Cys Ser Ser Pro Lys Pro Ala Leu Arg
 290 295 300

Tyr Ala Ala Val Arg Thr Leu Asn Lys Val Ala Met Lys His Pro Ser
 305 310 315 320

Ala Val Thr Ala Cys Asn Leu Asp Leu Glu Asn Leu Ile Thr Asp Ser
 325 330 335

Asn Arg Ser Ile Ala Thr Leu Ala Ile Thr Thr Leu Leu Lys Thr Gly
 340 345 350

Ser Glu Ser Ser Val Asp Arg Leu Met Lys Gln Ile Ser Ser Phe Val
 355 360 365

Ser Glu Ile Ser Asp Glu Phe Lys Val Val Val Val Gln Ala Ile Ser
 370 375 380

Ala Leu Cys Gln Lys Tyr Pro Arg Lys His Ser Val Met Met Thr Phe
 385 390 395 400

Leu Ser Asn Met Leu Arg Asp Asp Gly Gly Phe Glu Tyr Lys Arg Ala
 405 410 415

Ile Val Asp Cys Ile Ile Ser Ile Val Glu Glu Asn Pro Glu Ser Lys
 420 425 430

Glu Ala Gly Leu Ala His Leu Cys Glu Phe Ile Glu Asp Cys Glu His
 435 440 445

Thr Val Leu Ala Thr Lys Ile Leu His Leu Leu Gly Lys Glu Gly Pro
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450

455

460

Arg Thr Pro Val Pro Ser Lys Tyr Ile Arg Phe Ile Phe Asn Arg Val
 465 470 475 480

Val Leu Glu Asn Glu Ala Val Arg Ala Ala Ala Val Ser Ala Leu Ala
 485 490 495

Lys Phe Gly Ala Gln Asn Glu Ser Leu Leu Pro Ser Ile Leu Val Leu
 500 505 510

Leu Gln Arg Cys Met Met Asp Thr Asp Asp Glu Val Arg Asp Arg Ala
 515 520 525

Thr Phe Tyr Leu Asn Val Leu Gln Gln Arg Gln Met Ala Leu Asn Ala
 530 535 540

Thr Tyr Ile Phe Asn Gly Leu Thr Val Ser Val Pro Gly Met Glu Lys
 545 550 555 560

Ala Leu His Gln Tyr Thr Leu Glu Pro Ser Glu Lys Pro Phe Asp Met
 565 570 575

Lys Ser Ile Pro Leu Ala Met Ala Pro Val Phe Glu Gln Lys Ala Glu
 580 585 590

Ile Thr Leu Val Ala Thr Lys Pro Glu Lys Leu Ala Pro Ser Arg Gln
 595 600 605

Asp Ile Phe Gln Glu Gln Leu Ala Ala Ile Pro Glu Phe Leu Asn Ile
 610 615 620

Gly Pro Leu Phe Lys Ser Ser Glu Pro Val Gln Leu Thr Glu Ala Glu
 625 630 635 640

Thr Glu Tyr Phe Val Arg Cys Ile Lys His Met Phe Thr Asn His Ile
 645 650 655

Val Phe Gln Phe Asp Cys Thr Asn Thr Leu Asn Asp Gln Leu Leu Glu
 660 665 670

Lys Val Thr Val Gln Met Glu Pro Ser Asp Ser Tyr Glu Val Leu Ser
 675 680 685

Cys Ile Pro Ala Pro Ser Leu Pro Tyr Asn Gln Pro Gly Ile Cys Tyr
 690 695 700

Thr Leu Val Arg Leu Pro Asp Asp Asp Pro Thr Ala Val Ala Gly Ser
705 710 715 720

Phe Ser Cys Thr Met Lys Phe Thr Val Arg Asp Cys Asp Pro Asn Thr
725 730 735

Gly Val Pro Asp Glu Asp Gly Tyr Asp Asp Glu Tyr Val Leu Glu Asp
740 745 750

Leu Glu Val Thr Val Ser Asp His Ile Gln Lys Val Leu Lys Pro Asn
755 760 765

Phe Ala Ala Ala Trp Glu Glu Val Gly Asp Thr Phe Glu Lys Glu Glu
770 775 780

Thr Phe Ala Leu Ser Ser Thr Lys Thr Leu Glu Glu Ala Val Asn Asn
785 790 795 800

Ile Ile Thr Phe Leu Gly Met Gln Pro Cys Glu Arg Ser Asp Lys Val
805 810 815

Pro Glu Asn Lys Asn Ser His Ser Leu Tyr Leu Ala Gly Ile Phe Arg
820 825 830

Gly Gly Tyr Asp Leu Leu Val Arg Ser Arg Leu Ala Leu Ala Asp Gly
835 840 845

Val Thr Met Gln Val Thr Val Arg Ser Lys Glu Arg Thr Pro Val Asp
850 855 860

Val Ile Leu Ala Ser Val Gly
865 870

<210> 25

<211> 1900

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 25

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ttccctgtat actgtcaaag ccacccctgat tctggacaat gatggagatc gactttttgc 120

caagtactat gacgacacct accccagtgt caaggagcaa aaggcctttg agaagaacat 180

tttcaacaag acccatcgga ctgacagtga aattgccctc ttggaaggcc tgacagtggc 240

atacaaaagc agtatagatc tctattttcta tgtgattggc agctcctatg aaaatgagct 300

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| | |
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| tgtagaaaag cgagcactgc tggagaacat ggaggggctg ttcttggctg tggatgaaat | 420 |
| tgtagatgga ggggtgatcc tagagagtga tccccagcag gtggtacacc ggggtggcatt | 480 |
| aaggggtgaa gatgtcccc ttacggagca gaccgtgtct caggtgctgc agtcagccaa | 540 |
| agaacagatc aagtggtcac tccttcggtg aagacctcac tgttcctggc tcttcacct | 600 |
| cttcaaaaaa tttgcatgtc tgctgtgaat tttcatctag ttccccaatc gatgctctca | 660 |
| gggtcatctc ggggatcaca gggatcctta aatctccatt ctgtttgtgg ttgccccctc | 720 |
| aacctcccc acacccttcc tattcttttt cattcttctt gcagttctgg gagtaaagct | 780 |
| cccagcatat ttagataata gggcagggga agcaccctct ttctttctag actggattat | 840 |
| gctcacatgc tcccttgccc tgacattttt gtaaattctg tgccctttgc tgtagctaca | 900 |
| cttcagatta aagtaggaga aagaatgtgc tgagtgtttt cctccctttg cctctacctg | 960 |
| gccctcatcc caacagccca gcaaggggag agagaaagag aattcttttc tatagaacga | 1020 |
| gtgggggctg ggatgggtag ggatttatcc aatctaagcc ctaaccctac ttagtgacct | 1080 |
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| cccacttact aactgccagt tctccagcac tgaggtgggg cagataacgg ggcataattta | 1800 |
| agggggcatc tttgtgtaaa agatgcatgg agtcaggaga aaaccacctt cataaactgc | 1860 |
| tctgtgcaaa gaggaataaa acattttttc caaactgaaa | 1900 |

<210> 26

<211> 177

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 26

Met Glu Ala Leu Ile Leu Glu Pro Ser Leu Tyr Thr Val Lys Ala Ile
 1 5 10 15

Leu Ile Leu Asp Asn Asp Gly Asp Arg Leu Phe Ala Lys Tyr Tyr Asp
 20 25 30

Asp Thr Tyr Pro Ser Val Lys Glu Gln Lys Ala Phe Glu Lys Asn Ile
 35 40 45

Phe Asn Lys Thr His Arg Thr Asp Ser Glu Ile Ala Leu Leu Glu Gly
 50 55 60

Leu Thr Val Val Tyr Lys Ser Ser Ile Asp Leu Tyr Phe Tyr Val Ile
 65 70 75 80

Gly Ser Ser Tyr Glu Asn Glu Leu Met Leu Met Ala Val Leu Asn Cys
 85 90 95

Leu Phe Asp Ser Leu Ser Gln Met Leu Arg Lys Asn Val Glu Lys Arg
 100 105 110

Ala Leu Leu Glu Asn Met Glu Gly Leu Phe Leu Ala Val Asp Glu Ile
 115 120 125

Val Asp Gly Gly Val Ile Leu Glu Ser Asp Pro Gln Gln Val Val His
 130 135 140

Arg Val Ala Leu Arg Gly Glu Asp Val Pro Leu Thr Glu Gln Thr Val
 145 150 155 160

Ser Gln Val Leu Gln Ser Ala Lys Glu Gln Ile Lys Trp Ser Leu Leu
 165 170 175

Arg

<210> 27

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 27

Cys Glu Ser Gly Glu Leu Lys Pro Glu Asp Asp Val Thr Val Gly Pro
 1 5 10 15

Ala Gln Lys

<210> 28
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 28

Gly Asn Met Phe Ala Asn Leu Phe Lys Gly Leu Phe Gly Lys Lys Glu
 1 5 10 15

<210> 29
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 29

Glu Lys Lys Gly Phe Leu Gly Lys Phe Leu Asn Ala Phe Met Asn Gly
 1 5 10 15

<210> 30
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 30

Cys Thr His Pro Phe Thr His Glu Cys Gly Gly Gly Ser
 1 5 10

<210> 31
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 31

Cys Gly Glu His Val Arg Pro Ser Cys Gly Gly Gly Ser
 1 5 10

<210> 32
 <211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 32

Cys Asn Asn Thr Arg Ser Pro Tyr Cys Gly Gly Gly Ser
 1 5 10

<210> 33

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 33

Cys Glu Gln Thr Leu Tyr Arg Val Cys Gly Gly Gly Ser
 1 5 10

<210> 34

<211> 3916

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 34

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gagtgcgggc gcgccccacc accgccctca ccatggtgct gttggcagca gcggtctgca      180
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| atatggaaag tgtacatatg aagattgaag aaaagataac attaacctgt ggacgagacg | 1020 |
| gaggattaca gaatatggag ttgcatggca tgatcatgct taggatctca gatgacaagt | 1080 |
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<210> 35

<211> 511

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 35

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Met Val Leu Leu Ala Ala Ala Val Cys Thr Lys Ala Gly Lys Ala Ile
1           5           10          15

```

```

Val Ser Arg Gln Phe Val Glu Met Thr Arg Thr Arg Ile Glu Gly Leu
          20          25          30

```

```

Leu Ala Ala Phe Pro Lys Leu Met Asn Thr Gly Lys Gln His Thr Phe
          35          40          45

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Val Glu Thr Glu Ser Val Arg Tyr Val Tyr Gln Pro Met Glu Lys Leu
50 55 60

Tyr Met Val Leu Ile Thr Thr Lys Asn Ser Asn Ile Leu Glu Asp Leu
65 70 75 80

Glu Thr Leu Arg Leu Phe Ser Arg Val Ile Pro Glu Tyr Cys Arg Ala
85 90 95

Leu Glu Glu Asn Glu Ile Ser Glu His Cys Phe Asp Leu Ile Phe Ala
100 105 110

Phe Asp Glu Ile Val Ala Leu Gly Tyr Arg Glu Asn Val Asn Leu Ala
115 120 125

Gln Ile Arg Thr Phe Thr Glu Met Asp Ser His Glu Glu Lys Val Phe
130 135 140

Arg Ala Val Arg Glu Thr Gln Glu Arg Glu Ala Lys Ala Glu Met Arg
145 150 155 160

Arg Lys Ala Lys Glu Leu Gln Gln Ala Arg Arg Asp Ala Glu Arg Gln
165 170 175

Gly Lys Lys Ala Pro Gly Phe Gly Gly Phe Gly Ser Ser Ala Val Ser
180 185 190

Gly Gly Ser Thr Ala Ala Met Ile Thr Glu Thr Ile Ile Glu Thr Asp
195 200 205

Lys Pro Lys Val Ala Pro Ala Pro Ala Arg Pro Ser Gly Pro Ser Lys
210 215 220

Ala Leu Lys Leu Gly Ala Lys Gly Lys Glu Val Asp Asn Phe Val Asp
225 230 235 240

Lys Leu Lys Ser Glu Gly Glu Thr Ile Met Ser Ser Ser Met Gly Lys
245 250 255

Arg Thr Ser Glu Ala Thr Lys Met His Ala Pro Pro Ile Asn Met Glu
260 265 270

Ser Val His Met Lys Ile Glu Glu Lys Ile Thr Leu Thr Cys Gly Arg
275 280 285

Asp Gly Gly Leu Gln Asn Met Glu Leu His Gly Met Ile Met Leu Arg
290 295 300

Ile Ser Asp Asp Lys Tyr Gly Arg Ile Arg Leu His Val Glu Asn Glu
305 310 315 320

Asp Lys Lys Gly Val Gln Leu Gln Thr His Pro Asn Val Asp Lys Lys
325 330 335

Leu Phe Thr Ala Glu Ser Leu Ile Gly Leu Lys Asn Pro Glu Lys Ser
340 345 350

Phe Pro Val Asn Ser Asp Val Gly Val Leu Lys Trp Arg Leu Gln Thr
355 360 365

Thr Glu Glu Ser Phe Ile Pro Leu Thr Ile Asn Cys Trp Pro Ser Glu
370 375 380

Ser Gly Asn Gly Cys Asp Val Asn Ile Glu Tyr Glu Leu Gln Glu Asp
385 390 395 400

Asn Leu Glu Leu Asn Asp Val Val Ile Thr Ile Pro Leu Pro Ser Gly
405 410 415

Val Gly Ala Pro Val Ile Gly Glu Ile Asp Gly Glu Tyr Arg His Asp
420 425 430

Ser Arg Arg Asn Thr Leu Glu Trp Cys Leu Pro Val Ile Asp Ala Lys
435 440 445

Asn Lys Ser Gly Ser Leu Glu Phe Ser Ile Ala Gly Gln Pro Asn Asp
450 455 460

Phe Phe Pro Val Gln Val Ser Phe Val Ser Lys Lys Asn Tyr Cys Asn
465 470 475 480

Ile Gln Val Thr Lys Val Thr Gln Val Asp Gly Asn Ser Pro Val Arg
485 490 495

Phe Ser Thr Glu Thr Thr Phe Leu Val Asp Lys Tyr Glu Ile Leu
500 505 510

<210> 36

<211> 65

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 36

Trp Gln Cys Ser Ala Cys Phe His Glu Asn Met Ser Ser Asp Ser Asn
1 5 10 15

Cys Ile Ser Cys Ser Ala Val Lys Pro Arg Pro Thr Glu Thr Ser Lys
20 25 30

Lys Leu Pro Ala Ser Pro Pro Ser Ser Asn Thr Lys Ser Thr Val Pro
35 40 45

Leu Ser Ser Thr Pro Gly Leu Gly Asp Ile Phe Lys Lys Pro Ala Gly
50 55 60

Met
65

<210> 37
<211> 70
<212> PRT
<213> Artificial Sequence

<220> Description of Artificial Sequence: Note = Synthetic Construct

<400> 37

Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys Ala Glu Val Thr Lys
1 5 10 15

Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr Cys Ile Lys Ala Thr
20 25 30

Leu Leu Ile Pro Ser Thr Thr Lys Ser Ile Asn Pro Ala Thr Asn Thr
35 40 45

Leu Ala Phe Ala Ser Cys Ser Ala Ser Ile Pro Asn Glu Glu Met Phe
50 55 60

Lys Lys Pro Met Gly Ser
65 70

<210> 38
<211> 52
<212> PRT
<213> Artificial Sequence

<220> Description of Artificial Sequence: Note = Synthetic Construct

<400> 38

Trp Glu Cys Thr Val Cys His Met Gln Asn Lys Thr Glu Asp Asn Thr
1 5 10 15

Cys Val Gly Cys Lys Ala Glu Lys Pro Gly Thr Val Lys Ser Val Pro
20 25 30

Thr Ala Ala Pro Ser Gly Leu Leu Gly Leu Leu His Gln Phe Lys Lys
35 40 45

Pro Thr Gly Ser
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<210> 39
<211> 64
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 39

Trp Asp Cys Asp Val Cys Leu Ile Gln Asn Lys Pro Glu Ala Ala Lys
1 5 10 15

Cys Ile Ala Cys Glu Ser Ala Lys Pro Gly Thr Lys Ala Glu Pro Lys
20 25 30

Gly Thr Phe Asp Thr Val Lys Asn Ser Val Ser Val Ala Pro Leu Ser
35 40 45

Ser Gly Gln Leu Gly Leu Leu Asp Gln Phe Lys Lys Ser Ala Gly Ser
50 55 60

<210> 40
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 40

Trp Asp Cys Asp Val Cys Leu Val Glu Asn Lys Pro Glu Ala Thr Lys
1 5 10 15

Cys Val Ala Cys
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<210> 41
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 41

His Val Leu Glu Gly His Asp Arg
1 5

<210> 42
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 42

His Val Leu Glu Gly His Asp Arg
1 5

<210> 43
<211> 8
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<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 43

Asp Val Ala Val Met Gln Leu Arg
1 5

<210> 44
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 44

Asp Val Ala Val Met Gln Leu Arg
1 5

<210> 45
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 45

Ala Ser Asn Leu Glu Asn Ser Thr Tyr Asp Leu Tyr Thr Ile Pro Lys
1 5 10 15

<210> 46
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 46

Ala Ser Asn Leu Glu Asn Ser Thr Tyr Asp Leu Tyr Thr Ile Pro Lys
 1 5 10 15

<210> 47
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 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 47

Ser Ser Gly Leu Thr Ala Val Trp Val Ala Arg
 1 5 10

<210> 48
 <211> 11
 <212> PRT
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<220>
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<400> 48

Ser Ser Gly Leu Thr Ala Val Trp Val Ala Arg
 1 5 10

<210> 49
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 49

Thr Leu Asp Leu Pro Ile Tyr Leu Thr Arg
 1 5 10

<210> 50
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<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct
 <400> 50

Thr Leu Asp Leu Pro Ile Tyr Val Thr Arg
 1 5 10

<210> 51
 <211> 12
 <212> PRT
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<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct
 <400> 51

Leu Val Gly Gln Ser Ile Ile Ala Tyr Leu Gln Lys
 1 5 10

<210> 52
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 <212> PRT
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<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct
 <400> 52

Leu Val Gly Gln Ser Ile Ile Ala Tyr Leu Gln Lys
 1 5 10

<210> 53
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 <212> PRT
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<220>
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 <400> 53

Leu Ser Phe Leu Tyr Leu Ile Thr Gly Asn Leu Glu Lys
 1 5 10

<210> 54
 <211> 13
 <212> PRT
 <213> Artificial Sequence

<220>
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 <400> 54

Val Ser Phe Leu Tyr Leu Ile Thr Gly Asn Leu Glu Lys
 1 5 10

<210> 55
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 <212> PRT
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<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 55

Glu Tyr Ile Val Gly Leu Ser Met Glu Ile Asp Arg
 1 5 10

<210> 56
 <211> 12
 <212> PRT
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<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 56

Glu Tyr Ile Val Gly Leu Ser Val Glu Thr Glu Arg
 1 5 10

<210> 57
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<220>
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<400> 57

Thr Ala Val Asn Leu Phe Phe Lys
 1 5

<210> 58
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<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 58

Thr Ala Leu Asn Leu Phe Phe Lys
 1 5

<210> 59
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 59

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Thr | Val | Thr | Glu | Ile | Gly | Lys | Asp | Val | Ile | Gly | Leu | Arg |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |

<210> 60

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 60

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Thr | Thr | Val | Thr | Glu | Ile | Gly | Lys | Asp | Val | Ile | Gly | Leu | Arg |
| 1 | | | | 5 | | | | | 10 | | | | 15 | |

<210> 61

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 61

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Thr | Pro | Asp | Leu | Glu | Val | Arg |
| 1 | | | | 5 | | | | | 10 |

<210> 62

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 62

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Thr | Pro | Asp | Leu | Glu | Val | Arg |
| 1 | | | | 5 | | | | | 10 |

<210> 63

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 63

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ser | Gly | Glu | Leu | Lys | Pro | Glu | Asp | Asp | Val | Thr | Val | Gly | Pro | Ala |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |

Gln Lys

<210> 64
 <211> 18
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 64

Glu Ala Gly Glu Leu Lys Pro Glu Glu Glu Ile Thr Val Gly Pro Val
 1 5 10 15

Gln Lys

<210> 65
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 65

Val Phe Asn Tyr Asn Thr Leu Glu Arg
 1 5

<210> 66
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 66

Val Phe Asn Tyr Asn Thr Leu Glu Arg
 1 5

<210> 67
 <211> 10
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 67

His Ser Glu Ile Gln Gln Ala Asn Leu Lys

1

5

<210> 68
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct
<400> 68

His Ser Glu Val Gln Gln Ala Asn Leu Lys
1 5 10

<210> 69
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct
<400> 69

Leu Pro Glu Ala Ala Phe Leu Ala Arg
1 5

<210> 70
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct
<400> 70

Leu Pro Glu Ala Ala Phe Leu Ala Arg
1 5

<210> 71
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct
<400> 71

Thr Tyr Leu Pro Ser Gln Val Ser Arg
1 5

<210> 72
<211> 9
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 72

Thr Tyr Leu Pro Ser Gln Val Ser Arg
1 5

<210> 73

<211> 65

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 73

Phe Gly Leu Trp Gln Cys Ser Ala Cys Phe His Glu Asn Met Ser Ser
1 5 10 15

Asp Ser Asn Cys Thr Ser Cys Ser Ala Val Lys Pro Arg Pro Thr Glu
20 25 30

Thr Ser Lys Lys Leu Pro Ala Ser Pro Pro Ser Ser Asn Thr Lys Ser
35 40 45

Thr Val Pro Leu Ser Ser Thr Pro Gly Leu Gly Asp Ile Phe Lys Lys
50 55 60

Pro
65

<210> 74

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 74

Ala Gly Met Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys Ala Glu
1 5 10 15

Val Thr Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr Cys Ile
20 25 30

Lys Ala Thr Leu Leu Ile Pro Ser Thr Thr Lys Ser Ile Asn Pro Ala
35 40 45

Thr Asn Thr Leu Ala Phe Ala Ser Cys Ser Ala Ser Ile Pro Asn Glu
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50

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55 60

Glu Met Phe Lys Lys Pro
65 70

<210> 75
<211> 53
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 75

Met Gly Ser Trp Glu Cys Thr Val Cys His Met Gln Asn Lys Thr Glu
1 5 10 15

Asp Asn Thr Cys Val Gly Cys Lys Ala Glu Asp Lys Pro Gly Thr Val
20 25 30

Lys Thr Val Pro Thr Ala Ala Pro Ser Gly Leu Leu Gly Leu Leu His
35 40 45 50

Gln Phe Lys Lys Pro
50

<210> 76
<211> 64
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 76

Thr Gly Ser Trp Asp Cys Asp Val Cys Leu Ile Gln Asn Lys Pro Glu
1 5 10 15

Ala Ala Lys Cys Ile Ala Cys Glu Ser Ala Lys Pro Gly Thr Lys Ala
20 25 30

Glu Pro Lys Gly Thr Phe Asp Thr Val Lys Asn Ser Val Ser Val Ala
35 40 45

Pro Leu Ser Ser Gly Gln Leu Gly Leu Leu Asp Gln Phe Lys Lys Ser
50 55 60

<210> 77
<211> 64
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 77

Gly Ser Ser Trp Gln Cys Asp Thr Cys Leu Leu Gln Asn Lys Val Thr
 1 5 10 15

Asp Asn Lys Cys Ile Ala Cys Gln Ala Ala Lys Leu Ser Pro Arg Asp
 20 25 30

Thr Ala Lys Gln Thr Gly Ile Glu Thr Pro Asn Lys Ser Gly Lys Thr
 35 40 45

Thr Leu Ser Ala Ser Gly Thr Gly Phe Gly Asp Lys Phe Lys Pro Val
 50 55 60

<210> 78

<211> 71

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 78

Ile Gly Thr Trp Asp Cys Asp Thr Cys Leu Val Gln Asn Lys Pro Glu
 1 5 10 15

Ala Ile Lys Cys Val Ala Cys Glu Thr Pro Lys Pro Gly Thr Cys Val
 20 25 30

Lys Arg Ala Leu Thr Leu Thr Val Val Ser Glu Ser Ala Glu Thr Met
 35 40 45

Thr Ala Ser Ser Ser Ser Cys Thr Val Thr Thr Gly Thr Leu Gly Phe
 50 55 60

Gly Asp Lys Phe Lys Arg Pro
 65 70

<210> 79

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 79

Ile Gly Ser Trp Glu Cys Ser Val Cys Cys Val Ser Asn Asn Ala Glu
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1 5 10 15

Asp Asn Lys Cys Val Ser Cys Met Ser Glu Lys Pro Gly Ser Ser Val
20 25 30

Pro Ala Ser Ser Ser Ser Thr Val Pro Val Ser Leu Pro Ser Gly Gly
35 40 45

Ser Leu Gly Leu Glu Lys Phe Lys Lys Pro
50 55

<210> 80

<211> 69

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 80

Glu Gly Ser Trp Asp Cys Glu Leu Cys Leu Val Gln Asn Lys Ala Asp
1 5 10 15

Ser Thr Lys Cys Leu Ala Cys Glu Ser Ala Lys Pro Gly Thr Lys Ser
20 25 30

Gly Phe Lys Gly Phe Asp Thr Ser Ser Ser Ser Ser Asn Ser Ala Ala
35 40 45

Ser Ser Ser Phe Lys Phe Gly Val Ser Ser Ser Ser Ser Gly Pro Ser
50 55 60

Gln Thr Leu Thr Ser
65

<210> 81

<211> 63

<212> PRT

<213> Artificial sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 81

Gly Ser Trp Trp His Cys Asn Ser Cys Ser Leu Lys Asn Ala Ser Thr
1 5 10 15

Ala Lys Lys Cys Val Ser Cys Gln Asn Leu Asn Pro Ser Asn Lys Glu
20 25 30

Leu Val Gly Pro Pro Leu Ala Glu Thr Val Phe Thr Pro Lys Thr Ser
 35 40 45

Pro Glu Asn Val Gln Asp Arg Phe Ala Leu Val Thr Pro Lys Lys
 50 55 60

<210> 82

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 82

Glu Gly His Trp Asp Cys Ser Ile Cys Leu Val Arg Asn Glu Pro Thr
 1 5 10 15

Val Ser Arg Cys Ile Ala Cys Gln Asn Thr Lys Ser Ala Asn Lys Ser
 20 25 30

Gly Ser Ser Phe Val His Gln Ala Ser Phe Lys Phe Gly Gln Gly Asp
 35 40 45

Leu Pro Lys Pro Ile Asn Ser Asp Phe Arg Ser Val Phe Ser Thr Lys
 50 55 60

<210> 83

<211> 64

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 83

Glu Gly Gln Trp Asp Cys Ser Ala Cys Leu Val Gln Asn Glu Gly Ser
 1 5 10 15

Ser Thr Lys Cys Ala Ala Cys Gln Asn Pro Arg Lys Gln Ser Leu Pro
 20 25 30

Ala Thr Ser Ile Pro Thr Pro Ala Ser Phe Lys Phe Gly Thr Ser Glu
 35 40 45

Thr Ser Lys Thr Leu Lys Ser Gly Phe Glu Asp Met Phe Ala Lys Lys
 50 55 60

<210> 84

<211> 63

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 84

Glu Gly Gln Trp Asp Cys Ser Ser Cys Leu Val Arg Asn Glu Ala Asn
1 5 10 15

Ala Thr Arg Cys Val Ala Cys Gln Asn Pro Asp Lys Pro Ser Pro Ser
20 25 30

Thr Ser Val Pro Ala Pro Ala Ser Phe Lys Phe Gly Thr Ser Glu Thr
35 40 45

Ser Lys Ala Pro Lys Ser Gly Phe Glu Gly Met Phe Thr Lys Lys
50 55 60

<210> 85

<211> 59

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 85

Glu Gly Gln Trp Asp Cys Ser Val Cys Leu Val Arg Asn Glu Ala Ser
1 5 10 15

Ala Thr Lys Cys Ile Ala Cys Gln Asn Pro Gly Lys Gln Asn Gln Thr
20 25 30

Thr Ser Ala Val Ser Thr Pro Ala Ser Ser Glu Thr Ser Lys Ala Pro
35 40 45

Lys Ser Gly Phe Glu Gly Met Phe Thr Lys Lys
50 55

<210> 86

<211> 59

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 86

Glu Gly Gln Trp Asp Cys Ser Val Cys Leu Val Arg Asn Glu Ala Ser
1 5 10 15

Ala Thr Lys Cys Ile Ala Cys Gln Asn Pro Gly Lys Gln Asn Gln Thr
 20 25 30

Thr Ser Ala Val Ser Thr Pro Ala Ser Ser Glu Thr Ser Lys Ala Pro
 35 40 45

Lys Ser Gly Phe Glu Gly Met Phe Thr Lys Lys
 50 55

<210> 87

<211> 57

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 87

Glu Gly Gln Trp Asp Cys Ser Val Cys Leu Val Arg Asn Glu Ala Ser
 1 5 10 15

Ala Thr Lys Cys Ile Ala Cys Gln Cys Pro Ser Lys Gln Asn Gln Thr
 20 25 30

Thr Ala Ile Ser Thr Pro Ala Ser Ser Glu Ile Ser Lys Ala Pro Lys
 35 40 45

Ser Gly Phe Glu Gly Met Phe Ile Arg
 50 55

<210> 88

<211> 70

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 88

Lys Gly Gln Trp Asp Cys Ser Val Cys Cys Val Gln Asn Glu Ser Ser
 1 5 10 15

Ser Leu Lys Cys Val Ala Cys Asp Ala Ser Lys Pro Thr His Lys Pro
 20 25 30

Ile Ala Glu Ala Pro Ser Ala Phe Thr Leu Gly Ser Glu Met Lys Leu
 35 40 45

His Asp Ser Ser Gly Ser Gln Val Gly Thr Gly Phe Lys Ser Asn Phe
 50 55 60

Ser Glu Lys Ala Ser Lys
65 70

<210> 89
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct
<400> 89

Met Trp Ala Cys Gln His Cys Thr Phe Met Asn Gln Pro Gly Thr Gly
1 5 10 15

His Cys Glu Met Cys Ser Leu Pro Arg Thr
20 25

<210> 90
<211> 37
<212> PRT
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<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct
<400> 90

Glu Gly Trp Asp Cys Ser Val Cys Leu Val Asn Glu Ala Ser Ala Thr
1 5 10 15

Lys Cys Ile Ala Cys Gln Pro Lys Thr Ala Ser Ala Ser Ser Ala
20 25 30

Ser Phe Met Phe Lys
35

<210> 91
<211> 7
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Note = Synthetic Construct
<400> 91

Thr His Pro Phe Thr His Glu
1 5

<210> 92
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct
 <400> 92

Thr His Pro Phe Thr His Glu
 1 5

<210> 93
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Note = Synthetic Construct
 <400> 93

Thr His Pro Phe Thr His Glu
 1 5

<210> 94
 <211> 7
 <212> PRT
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<220>
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Ser Ser Phe Ala His Ser Arg
 1 5

<210> 95
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 <212> PRT
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<220>
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Ser Ser Phe Ala His Ser Arg
 1 5

<210> 96
 <211> 7
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<220>
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Gly Glu His Val Arg Pro Ser

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<210> 97
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 <400> 97

Gly Glu His Val Arg Pro Ser
 1 5

<210> 98
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>
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Pro Gly Pro His Leu Pro His
 1 5

<210> 99
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 <212> PRT
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<220>
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Tyr Asn Asn Gln His Leu Thr
 1 5

<210> 100
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Leu Ala His His Gly Thr Leu
 1 5

<210> 101
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<220>
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<400> 101

Val Gln His Asn Ala Arg Ser
1 5

<210> 102
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<212> PRT
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<400> 102

Thr Ala Ser Leu His Phe Ser
1 5

<210> 103
<211> 7
<212> PRT
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<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 103

Lys Pro Asp Ser Met Pro Trp
1 5

<210> 104
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 104

Ser Arg Thr Thr Ser Ser Trp
1 5

<210> 105
<211> 7
<212> PRT
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 105

Gly Pro Gln Ser Ala Lys Thr

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5

<210> 106

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Note = Synthetic Construct

<400> 106

Asn Leu Gln Ala Arg Gly Tyr

1

5